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US-09-825-212-1
                                                                                                                                                                                September 15, 2004, 12:20:54; Search time 135 Seconds (without alignments) 760.153 Million cell updates/sec
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1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHHH 320
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
3: cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1335176 seqs, 320689617 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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SUMMARIES	ΩΙ	US-09-825-212-1	US-09-925-637-14	US-10-084-205-14	US-10-712-713-14	US-10-787-887-2	US-10-032-201B-265	US-10-787-887-10	US-10-290-072-66	US-10-141-531-66	US-10-032-2018-198	US-10-032-201B-235	US-10-290-072-103	US-10-290-0139	US-10-141-531-103	US-10-141-531-139	
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	Query Match Length DB	320	312	312	312	311	311	310	315	315	315	315	316	316	316	316	
о¥о	Query Match	100.0	95.8	95.8	95.8	95.2	93.9	87.4	69.4	69.4	69.4	68.8	68.8	68.8	68.9	68.8	
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US-10-290-072-148	41-531-1	-10-290-07	-10-290-072-1	10-141-531-8	-10-141-531-1	-10-290-072-	-10-141-531-1	-10-29	10-290-072-15	10-290-072-1	10-141-53	10-141-531-1	10-141-531-17	10-290-072-9	10 - 29	10-290-072-19	10-141-531-	1-531-1	-10-141-531-19	-10-290-072-16	10-141-531-16	-10-290-072-2	-10-141-531-20	-10-032-20	-10-032-201B-2	-10-032-201B-2	.0-032-201B-2	.0 - 032 - 2	US-10-032-201B-208
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## ALIGNMENTS

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61 GPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
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US-09-08-25-212-1
; Sequence 1, Application US/08925212
; Sequence 1, Application US/08925212
; Publication No. US20030166843A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Timothy E
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS THIOREDOXIN REDUCTASE
; TITLE REFERENCE: 00032.US1
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/195,055
; PRIOR APPLICATION NUMBER: 60/195,055
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 320
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100.0%; Pred. No. 5.5e-148;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Staphylococcus aureus
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Best Local Similarity 100.
Matches 320; Conservative
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 14
LENGTH: 312
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LENGTH: 312
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APPLICANT: Choi

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: BBS60

CURRENT APPLICATION NUMBER: US/09/925,637

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/23773

PRIOR FILING DATE: 1999-09-01

PRIOR FILING DATE: 1999-09-01

PRIOR FILING DATE: 1997-01-03

PRIOR FILING DATE: 1997-01-03

PRIOR PLING DATE: 1997-01-03

PRIOR PLING DATE: 1997-01-02

PRIOR PLING DATE: 1997-01-02

PRIOR FILING DATE: 1997-01-04

PRIOR FILING DATE: 1997-01-05

PRIOR FILING DATE: 1997-01-05

PRIOR FILING DATE: 1997-01-05

PRIOR PLING DATE: 1997-01-05

PRIOR PLING DATE: 1997-01-05

PRIOR PLING DATE: 1997-01-06

SOFTWARE: PATCHING DATE: 1996-01-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PATCHIN VEY: 2.0

SEQ ID NO 14

LENGTH: 312
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Pred. No. 1.7e-141;
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; Sequence 14, Application US/10084205
; Publication No. US20030049648A1
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Best Local Similarity 99.4%;
Matches 310; Conservative
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US-09-925-637-14
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241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
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TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REPRENCE: PB515P1
CURRENT APPLICATION NUMBER: US/10/712,713
CURRENT APPLICATION NUMBER: US/10/084,205
PRIOR RELING DATE: 2003-2.28
PRIOR FILING DATE: 2003-2.28
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
JERERAL INFORMATION: 3.

JERERAL INFORMATION: 3.

APPLICATION: Choi, Gil

TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB515P1

CURRENT APPLICATION NUMBER: US/10/084,205

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PACENTIN Ver. 3.1
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Pred. No. 1.7e-141;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 1593; DB 14;
Pred. No. 1.7e-141;
0; Mismatches 2;
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Sequence 14, Application US/10712713

Publication No. US20040082002A1

GENERAL INFORMATION:
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99.4%;
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Best Local Similarity 99.4%;
Matches 310; Conservative
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APPLICANT: Van Rooijen, Gijs
APPLICANT: Van Rooijen, Gijs
APPLICANT: Deckers, Harm
APPLICANT: Beckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Applicants, Steve
APPLICANT: Moloney, Maurice
ITLE OF INVENTION: MTHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
ITLE OF INVENTION: COMPOSITIONS
FILE REPRENCE: 38814 3518
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 265
LENOTH: 311
            243 PLIAPFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTAIGDGSIAAQSAA 302
                               242 PLTAPPKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 301
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Pred. No. 1.7e-138;
1; Mismatches 5;
                                                                                                                                                                                             Sequence 265, Application US/10032201B; Publication No. US20030167524A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/10787887; Publication No. US20040161809A1; GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair; APPLICANT: Borovok, Ilya; APPLICANT: Cohen, Gerald; APPLICANT: Uziel, Orit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Staphylococcus aureus US-10-032-201B-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.9%;
98.1%;
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Best Local Similarity 98.1
Matches 304; Conservative
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                                                                                                                        VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
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                                                   Gaps
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TITLE OF INVENTION: Recombinant Staphylococcus Thioredoxin Reductase
FILE REFERENCE: 85189-899
CURRENT APPLICATION NUMBER: US/10/787,887
CURRENT PILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/076,525
PRIOR PILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1999-03-02
RIOR FILING DATE: 1999-03-02
SPIOR FILING DATE: 1999-03-02
RIOR FILING DATE: 1999-03-02
SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
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Pred. No. 1.8e-140;
0; Mismatches 2; Indels 0
     Indels
     2
   0; Mismatches
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Publication No. US20040161809A1
GENERAL INFORMATION:
APPLICANT: Abaronowitz, Yair
APPLICANT: Borovok, 11ya
APPLICANT: Cohen, Gerald
APPLICANT: Uziel, Orit
APPLICANT: KAtz, Leonard
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; ORGANISM: Staphylococcus aureus
US-10-787-887-2
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310; Conservative
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Matches 308; Conservative
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VESULT 9: 1141-531-66

Sequence 66, Application US/10141531

Sequence 66, Application US/10141531

Sequence 66, Application No. US20030100743A1

Sequence 66, Application No. US20030100743A1

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.

APPLICANT: Bright K.

APPLICANT: Desjarlais, John R.

APPLICANT: Luginbuhl, Peter

APPLICANT: Huginbuhl, Peter

APPLICANT: Huginbuhl, Peter

APPLICANT: Muchhal, Umesh

TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity

FILE REFERENCE: A-71457-2/RRN/RMK

CURRENT FILING DATE: 2002-05-06

FRIOR APPLICATION NUMBER: US 60/289,029

PRIOR APPLICATION NUMBER: US 60/289,029

PRIOR APPLICATION NUMBER: US 60/289,029

PRIOR APPLICATION NUMBER: US 60/289,029

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn version 3.1

SEQ ID NO 66
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Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55;
                                                                                                ; Score 1154; DB 12;
; Pred. No. 3.9e-100;
33; Mismatches 55;
                                                                                                     Query Match 69.4%; Best Local Similarity 71.4%; Matches 220; Conservative 3
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                TYPE: PRT CRGANISM: Bacillus subtilis US-10-290-072-66
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APPLICANT: Dalmia, John R.
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Heifetz, Peter
APPLICANT: Heifetz, Peter
APPLICANT: Holibulh, Peter
APPLICANT: Muchhal, Umesh
TITLE REPERBENCE: A.71457-3
CURRENT PAPLICATION NUMBER: US/10/290,072
CURRENT PILING DATE: 2002-11-06
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-05-04
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APPLICANT: Katz, Leonard
TITLE OF INVENTION: Recombinant Staphylococcus Thioredoxin Reductase
FILE REFERENCE: 85189-899
CURRENT APPLICATION NUMBER: US/10/787,887
CURRENT FILING DATE: 2004-02-27
PRIOR PILING DATE: 1998-03-02
PRIOR PLICATION NUMBER: US 60/076,525
PRIOR PLICATION NUMBER: US 09/261,301
PRIOR APPLICATION NUMBER: US 09/261,301
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                               Length 310;
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87.4%; Score 1452; DB 16;
Best Local Similarity 89.9%; Fred. No. 3.2e-128;
Matches 277; Conservative 18; Mismatches 13;
                                                                                                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-10-787-887-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66, Application US/10290072 Publication No. US20030211511A1 GENERAL INFORMATION:
                                                                                                                                                                                                                              SOFTWARE: Patentin version 3.2
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DYITELKD 309
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LENGTH: 310
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APPLICANT: Deckers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmiaki, Steve
APPLICANT: Moloney, Maurice
APPLICANT: Moloney, Maurice
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 38814 3518
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 235
LENGTH: 315
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68.6%; Pred. No. 2.5e-99;
ive 38; Mismatches 60
                                ; Sequence 235, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
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Publication No. US20030211511A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bacillus halodurans US-10-032-201B-235
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APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
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Best Local Similarity 68.6%
Matches 216; Conservative
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APPLICANT:
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APPLICANT: Van Rooijen, Gijs
APPLICANT: Deckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Zapladhinski, Steve
APPLICANT: Dalmia, Murice
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: MURBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
                                LGGRGVSYCAVCDGAFFKGKELVVVGGGDSAVEEGVYLTRFASKVTIVHRRDKLRAQSIL 185
                                                                       187 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHBADGVFIYIGMKPLTA 246
                                                                                              LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
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Best Local Similarity 71.4°
Matches 220; Conservative
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ELQETLKT 313
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306 ELQETLKT 313
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APPLICANT: Bailings, Steven P.
APPLICANT: Dailing, Bipin K.
APPLICANT: Dailing, Bipin K.
APPLICANT: Designation, John R.
APPLICANT: Designation, John R.
APPLICANT: Designation, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Housinbuth, Peter
APPLICANT: Muchhal, Tweek
APPLICANT: Muchhal, Jumesh
TITLE OF INVENTION NUMBER: US/10/141,531
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
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70.1%; Pred. No. 2.8e-99;
tive 33; Mismatches 61;
                                                                                                          Score 1145; DB 12;
Pred. No. 2.8e-99;
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                                                  CTHER INFORMATION: Bacillus subtillis variant US-10-290-072-139
                                                                                                             Query Match
68.9%; Score 1145; D
Best Local Similarity 70.1%; Pred, No. 2.8e
Matches 220; Conservative 33; Mismatches
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TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 70.1%
Matches 220; Conservative
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Sequence 139, Application US/10290072
Publication No. US20030211511A1
GENERAL INFORMATION:
APPLICANT: Baligas, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbhil, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
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                                                                                                                                                                                                                                                                   OTHER INFORMATION: Bacillus subtillis variant
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CURRENT APPLICATION NUMBER: US/10/290,072

CURRENT PILING DATE: 2002-11-66

PRIOR PILING DATE: 2002-04-05

PRIOR PLICATION NUMBER: US 60/370,609

PRIOR PLICATION NUMBER: US 60/376,682

PRIOR PLICATION NUMBER: US 60/376,682

PRIOR PLING DATE: 2002-04-29

PRIOR PLING DATE: 2002-05-06

PRIOR PLING DATE: 2002-05-06

PRIOR PLING DATE: 2001-05-04

NUMBER: OF SEQ ID NOSE: 239

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NOS: 239

SECTION 0.339
  PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SEQ ID NO 103
LENGTH: 316
                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
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US-10-290-072-139
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APPLICANT: del Val, Greg
APPLICANT: del Val, Greg
APPLICANT: Delmia, John R.
APPLICANT: Delmia, John R.
APPLICANT: Delegarlais, John R.
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchal, Unesh
TILLE OF INVENTION: NUCleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/141,531
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
LENGTH: 316

LENGTH: 316
                                                         VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
                                                                                                                  181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG 240
GPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
                     61 GPELSNRWFEHARKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIG 120
                                                                           MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Bacillus subtillis variant
                                                                                                                                                                                                                                                                                                     Application US/10141531
o. US20030100743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 70.19
Matches 220; Conservative
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- proteín search, using sw model OM protein

Run on:

September 15, 2004, 12:16:13; Search time 32 Seconds (without alignments) 516.260 Million cell updates/sec

US-09-825-212-1

Perfect score:

1662 1 MGTEIDFDIAIIGAGPAGWT......AAEYIEHLNDQARSHHHHHH 320 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

DB DB Minimum | Maximum |

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/pcTUS\_COMB.pep:\* 1 0 M 4 G 6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMATO

SUMMARIES	Description		-134-0000-5514 Sequence 3512,	-328-352-8114 Sequence 5514,	-328-352-5678 Semica 611	-198-452A-331 Semience 3878,	-543-681A-5633	-598-747-25 Semience	-598-747-7 Semience	197	eonemes.	-489-039A-12096 Semience	-540-014-24 Semience 24 Apr	1849 Semionos 2007	-540-014-9 Germones	-386-729A-7 Comission 7	-598-747-27	-598-747-6 Semience 27,	-220-677A-2 Semience 2,	91A-28463 S	-352-6394 Semience 630	Semience 630E	-236-2706 Semistroe 2306	-134-001C-4570 Semions 4570	-107-5322-6559 Somions 550.	-543-68111-4490 Sommond 4400	-134-0017-5497 Somica 149	-107-532A-6420 Sequence 6420.
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æ	Query		56.6	7	36.5	35.7	35.0					34.2			•		29.9	29.5	9	27.4	27.3	7	27.0	9	9	5	22.2	8
	Score	1083	940	618	607	594	581	579.5	<u></u>	71.	569.5	68.	In.		•	513.5			œ	455	ഹ	Ŋ	•	443	436	415	369.5	00
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Seguence 31441. A						Segmence 11, Appl	200	200	Segmence 90 Appl		6169						Sequence 32853, A	
US-09-252-991A-31441	US-09-252-991A-31700	US-09-489-039A-13402	US-09-134-001C-2974	US-09-134-000C-5068	US-09-091-097-34	US-09-091-097-10	US-09-556-877-90	US-09-620-412C-90	US-09-410-568-90	US-09-598-419-90	US-09-328-352-6168	US-09-252-991A-28041	US-09-262-856A-5	US-09-134-001C-3405	115-09-252-9918-25992	TIO OF THE POST OF THE	US-US-252-831A-32853	US-09-543-681A-5905
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199	215	192	553	334	507	507	474	474	474	474	496	456	491	473	479		005	484
17.2	16.8	16.4	15.2	14.3	14.1	14.0	13.5	13.5	13.5	13.5	13.1	12.9	12.8	12.6	12.6	10.0	7.7	12.0
285.5	279	273	253	238	234	233	225	225	225	225	218.5	215	212	210	210	200	1	199
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	1 !	45

## ALIGNMENTS

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Sequence 5512, Application US/09134001C
Patent No. 6380370
GERREAL INFORMATION:
GERREAL INFORMATION:
GERREAL INFORMATION:
GERREAL LAYN DOUGETCE-Stamm et al
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: GTC-OO;
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PELLOR DATE: 1999-08-13
PRIOR PELLOR DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
US-09-134-001C-5512
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TYPE: PRT (CRANISM: Staphylococcus epidermidis US-09-134-001C-5512

Length 253; 21; Indels 65.2%; Score 1083; DB 4; 85.7%; Pred. No. 5.5e-100; iive 14; Mismatches 21; Local Similarity 85.7 nes 209; Conservative Query Match Best Local S: Matches 209

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Gaps

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186 126 9 67 KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 음 ò à

246 69 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFLTKFADKVTIVHRRDELRAQNIL 128 QDRAFKUDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA g q δ

247 PFKDLGITNDVGXIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEXIE 306 à g

HLND 310 249 ELKD 252 307 à

RESULT 2 US-09-134-000C-5514 ; Sequence 5514, Application US/09134000C

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Sequence 5678, Application US/09328352
; Patent No. 6562958
; Patent No. 6562958
; Patent No. 6562958
; Faren No. 6562958
; TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                               188 DHLFVKEKEGKISIIWNHEVEEVLGDNTGVTSVRLKSTQDESKQDVEVHQLFVALGYKPN 247
                                                                                                                                                                                                                                    245 TAPFKDLGITNDVGYIVTKDDMT----TSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                                          248 TGMF-DGQLNLRDGYIQVQSGTSGNATATSVAGVFAAGDVADSIYRQAITSAGSGCMAAL 306
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68 MFBHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQEL 127
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                                  68 MOAHAERFGTELVYDHINEVDLNVRPFVLKGDMEEYTCDALIIATGATAQYLGLESEQNF
                                                                           128 GGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRILQ
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43.4%; Pred. No. 2.4e-52;
tive 55; Mismatches 110; Indels
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US-09-198-452A-331
Sequence 331, Application US/09198452A
Patent No. 6558294
GENERAL INFORMATION:
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US-09-328-352-5678
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US-09-328-352-5678
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTO9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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        PATENT NO. 6617156
GENERAL INFORMATION:
APPLICANT: LDND DOUGETE-Stamm et al
APPLICANT: LDND DOUGETE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1998-08-15
NUMBER OF SEQ ID NOS: 6812
SEQ ID NOS: 6812
SEQ ID NO 5514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
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37.2%; Score 618; DB 4; Length 317;
Best Local Similarity 44.1%; Pred. No. 1.9e-53;
Matches 137; Conservative 53; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                56.6%; Score 940; DB 4; ilarity 58.9%; Pred. No. 1.4e-85; Conservative 42; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HL 308
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US-09-328-352-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8114
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LQDRAFKNDKIDFIWSHTTKSINE---KDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
                 89 MEQHAEKFNTEIISDHINKVDLKNRPFRL--FGDEQEYTCDALIIATGASARYIGLPSEE 146
                                                                           243 PLTAPFKDLGITNDVGYIV----TKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDGSIA 297
                                                                                                                                                                                                             DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 RDELRAQRILQDRAFKNDKIDFIWSHTTKSINEK--DGK---VGSVTLTSTKDGSEETHE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09598747

Patent No. 6531648

GENERAL INFORMATION:
APPLICANT: Lanchan, Michael B.
APPLICANT: Desai, Nalini M.
APPLICANT: Gaadaska, Pamela Y.
TITLE OF INVENTION: GRADLE A-11383PI
FILE REFREENCE: A-11383PI
CURRENT PLIJNG DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 42
                                                                                                                                                     207 LIDRIMDKVKNGNIILHIDRILDEVLGDDMGVIKVRLKDIKSDKTEELEVMGVFIAIGHS
                                                    126 ELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKYTIVHRRDELRAQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|: | : :::|| : LITIFETTIFTETVIKVDFSSKPFKLFTDSKAILADAVILAIGAVAKWLSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GEQE-LGG---RGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 IAIIGAGPAGMTAAVYASRANLKTVMIERGI-----PGGQMANTEEVENFPGF-EMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 ADGVFIYIGMKPLTAPFKDLGITNDV-GYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 579.5; DB 4;
43.5%; Pred. No. 1.4e-49;
tive 50; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | :| | i | AAGTGCMAALDAEHYLQEIGSQ 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Arabidopsis thaliana
US-09-598-747-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.5:
Matches 140; Conservative
                                                                                                                                                                                                                                                             298 AQSAAEYIEHL 308
                                                                                                                                                                                                                                                                                              326 ALDAERYLDAL 336
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UDAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US 60/9/543,681A
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5633
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                    65 STRMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GEQELGGRGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKYTIVHRRDEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 GNDEFWQKGVTACAVCDGASPIFKNKDLYVIGGGDSALBEALYLTRYGSHVYVVHRRDKL 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 HKPNTDFLGGQLTLDESGYIVTEKGTSKTSVPGVFAAGDVQDKYYRQAVTSAGGGCIAAL 304
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                                                                                                                                                                                                                                                 35.7%; Score 594; DB 4; Length 311; 46.1%; Pred. No. 4.5e-51;
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                                                                                                                                                                                                                                                                                   42; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5633, Application US/09543681A
Patent No. 6605709
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                                                                                                                                                                          TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.1
Matches 141; Conservative
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Best Local 8
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22 TEBIYDLIIIGGGSAALSAGIYAGRAMMDTLIIEKDKIGGQVTTTSBIVNYPAIRHTTGP
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APPLICANT: Del Val, Greg
APPLICANT: Caillau, Maxime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                         298 AQSAAEYI 305
                                                                                                                                                                                                                                                                                                                                                                                               ATHAORYV 327
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BYTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BYTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT PAPPLICATION NUMBER: US/09/134,000C
CURRENT PAPPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1999-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATEURIN VEFSION 3.1
SEQ ID NO 3897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 DVVAELGVERDSMGYIKVDKEQRTNVEGVFAAGDCCDNPLKQVVTACGDGAVAAYSAYKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LVEEVEKRG-IPVHYSTTIRKI-IGSGKVEKVAYNREKKEBFEIEADGIFVALGMRPAT 237
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             APPLICANT: Lanahan, Michael B.
APPLICANT: Desai, Nalini M.
APPLICANT: Desai, Nalini M.
APPLICANT: Geadaska, Malini M.
TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USFUL
TITLE OF INVENTION: THEREIN
FILE REFERENCE: A-313981N A-313981N CURRENT APPLICATION NUMBER: US/09/598,747
CURRENT APPLICATION NUMBER: US/09/598,747
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 LQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHBADGVFIYIGMKPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YDVAIIGGGBAGLTAALYSARYGLKTVFFETVDPVSQLSLAARIENYPGFEG-SGMELLE
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                                                                                                                                                                                                                                                                                                                                           Length 300,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.4%; Score 571.5; DB 4; Length ilarity 39.0%; Pred. No. 8.6e-49; Conservative 58; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                           Query Match
34.6%; Score 575; DB 4; Length 30
Best Local Similarity 43.2%; Pred. No. 3.4e-49;
Matches 130; Conservative 53; Mismatches 112; Indels
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Patent No. 6617156
                                                                                                                                                                                                                                                                       TYPE: PRT CRGANISM: Archaeoglobus fulgidus US-09-598-747-7
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Best Local Similarity
Matches 120; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 LRAQRILQDRAFKNDKID--FIWSHTTKSINEKDGK---VGSVTLTSTKDGSE-ETHEAD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                        123 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                                                            183 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEAD-----GVFI 237
                                                                                                                                                                                                                             238 YIGMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIA 297
63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                             82 ELMBEMRIQAQDFGVAFTNDBIIDVDFSQTIKTVQSASQTYQAYAVLIATGASARKIGFP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGF-EM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Caillau, Maximus
APPLICANT: Lemauz, Peggy G.
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
ITILE OF INVENTION: Barley Gene for Thioredoxin and
ITILE OF INVENTION: NADP-Thioredoxin Reductase
ITILE OF INVENTION: NADP-Thioredoxin Reductase
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/127,740
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.3%; Score 569.5; DB 4; Best Local Similarity 42.1%; Pred. No. 1.3e-48; Matches 136; Conservative 55; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/09540014; Patent No. 6380372
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION WHERE: US 60/094,190
PRIOR APPLICATION WHERE: US 60/094,190
RECORD FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 DISTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 ELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKWLSFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GEQE-LGG----RGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 RDELRAQRILQDRAFKNDKIDFIWSHTTKSINEK--DGK---VGSVTLTSTKDGSEETHE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ADGVEIYIGMKPLTAPFKDLGITNDV-GYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                          9 IAIIGAGPAGWIAAVYASRANLKIVMIERGI-----PGGQMANTEEVENFPGF-EMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 IAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGF-EMITGPDLSTK
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                                                                                                                                                                                                                                                                                                                                                             Length 332;
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                                                                                                                                                                                                                                                                                                                                              Query Match 33.6%; Score 559; DB 4; L. Best Local Similarity 43.2%; Pred. No. 1.5e-47; Matches 139; Conservative 49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.1%; Score 549.5; DB 4;
40.3%; Pred. No. 1.3e-46;
Live 54; Mismatches 121;
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR APPLICATION NUMBER: US 60/17,740
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOUTHARRE: FASCSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AAGTGCMAALDAEHYLQEIGSQ 327
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                                                                                                                                                                                                                                                                                   GRGANISM: Arabidopsis thaliana US-09-540-014-24
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Best Local Similarity
Matches 124; Conserv
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US-09-252-991A-29849
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US-09-252-991A-29849
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION:

TITLE OF INVENTION:

PILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                  -TISVPGIFAAGDVRDKGLRQI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IGPDLSTKMFEHAKKFGAVYQYGDIKSVE------DKGEYKVINFGNKELFAKAVI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 İGPLIMBRIMHEHAAKFETEIIFDHİSRVDLQNRPFRLTGDSGEY-----TCDALI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 IATGAEYKKIGVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFAD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 KVTIVHRRDELRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGK---VGSVTLTSTKDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.2%; Score 568.5; DB 4; Length 40.7%; Pred. No. 1.9e-48; Ive 51; Mismatches 114; Indels
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APPLICANT: Del Val, Greg
APPLICANT: Del Val, Greg
APPLICANT: Del Val, Greg
APPLICANT: Lemauz, Peggy G.
APPLICANT: Demauz, Peggy G.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 RDKGLRQIVTATGDGSIAAQSAAEYIEHLNDQAR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 MDHIYRQAITSAGTGCMAALDAERYLDGLADACK 349
          GVFIYIGMKPLTAPFK-DLGITNDVGYIVTKDDM-
                                                                                                                                                                                                                             Sequence 12096, Application US/09489039A
Patent No. 6610836
                                                                                      288 VTATGDGSIAAQSAAEYIEHLND 310
                                                                                                              Sequence 24, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.7%
Matches 136; Conservative
                                                                                                                                                                                        RESULT 11
US-09-489-039A-12096
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obtainable from P. chrysogenum, the set of genes encoding the same and the use of oxido reductase enzyme systems or genes encoding the same for increasing antibiotic production
                                                        250 FPAIGHEPATKFLNGQLELHADGYVATKPGSTHTSVEGVFAAGDVQDKKYRQAITAAGSG 309
                                    236 FIYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDG 294
193 RASKIMQARALSNPKIQVVWD---SEVVEAYGGAGGPLAGVKVKNLVTGEVSDLQVSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/386,729A FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%; Score 513.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Weil, Gotshal & Manges
2882 Sand Hill Road, Ste. 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-7017-1994
FILING DATE: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
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APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          Van Der Voort, Lucia H.
Cohen, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          Bovenberg, Roelof A. L
Schreiber, Rachel
Argaman, Anat
Av-Gay, Yossef
Nan, Helena M.
                                                                                                                                                                                                                                                ; Sequence 7, Application US/08386729A; Patent No. 5753435; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kattevilder, Alfred
                                                                                                                                               310 CMAALDAEHYLQEVGAQ 326
                                                                                                                      295 SIAAQSAAEYIEHLNDQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pallissa, Harriet
                                                                                                                                                                                                                                                                                                            Aharonowitz, Yair
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" dli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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US-08-386-729A-7
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GEQELGGRGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTIKFADKVTIVHRRDEL 180
                                                                                                                                                                                                                       DRAFKNDKIDFIWSHTTKSINEKDGKVGSVT--LTSTKDGSEETHEADGVFIYIGMKPLT 245
                                                                                                                                                                                                                                                                                              246 APFKDLGITNDVGYIVTK----DDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
                                                                                                                                                                                                                                                                                                                    128 GGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRILQ 187
                                                                                                                                                                    68 MFBHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQEL 127
                                                                                             17 VIILGSGPAGYSAAVYAARANLKPLLITGMQAGGQLTTTTEVDNWPGDPHGLTGPALMQR 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lemauz, Peggy G.
APPLICANT: Lemauz, Bob B.
TITLE OF INVENTION: Barley Gene for Thioredoxin and TITLE OF INVENTION: NADP-Thioredoxin Reductase FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09540014
Patent No. 6380372
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Del Val, Greg
Caillau, Maxime
Lemauz, Peggy G.
Buchanan, Bob B.
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Best Local Similarity
Matches 124; Conserv
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APPLICANT:
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                                                                                        109 IIATGAEYKKIGVPGEQELGGRGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEFGTFTTK 166
                                                                   9 IAIIGAGPAGWTAAVXASRANLKTVMIERGI-----PGGQMANTEEVENFPGFEM-ITGP 62
Best Local Similarity 37.5%; Pred. No. 5.4e-43;
Matches 121; Conservative 54; Mismatches 115; Indels 33; Gaps
                                                                                                                                                                                        283 GLRQIVTATGDGSIAAQSAAEYI 305
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Search completed: September 15, 2004, 12:22:10 Job time: 33 secs

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us-09-825-212-1.rag

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2004, 12:05:48 ; Search time 125 Seconds (without alignments) 723.322 Million cell updates/sec Run on:

ниннинза US-09-825-212-1 1662 1 MGTEIDFDIAIIGAGPAGMT.....AABYIEHLNDQA Title: Perfect score: Sequence:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	ABB04148	AAU00834	ARM72250	ADARGEON	AAY29854	ABP60916	AAY29855	AAG82024	ARPEN849	AA020619	10000 E	AUD26553	AAU20627	ABF60886	ADD26570	ABP40667	ABP60863	ABB49968	ADB08826	ARP26879	COCKAGGK	ADD34256	ABF60904	ABP26878	ABP60919	ABU01907	ARDEDBOA	٦.
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728.5 726 706	697.5	647.5 645.5	645.5 644.5	639.5	635.5	632.5	632.5	632.5	0.00	0.220	0.250	632.5	629.5
26 27 28		31 32	0. 0. 4. 4.	35	36	7 8 7 8	39	40	7 C	7 7	7 5	*	45

## ALIGNMENTS

RESULT 1

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note= "Optional disulphide bond; formed when thioredoxin s reduced and broken when FAD is oxidised"
                                                                                                                                                                                                                                               315. .320 - -- /note= "Histidine tag; aids the purification of the protein"
                                                                                                                                                                                                               /label= NADPH_binding_site
                                                                                                                                                                                                                      .83. .289
|abel= NADPH_binding_site
                                                  label = NADPH_binding_site
                                                          56. .157
label= NADPH_binding_site
                                                                       .59. .161
'label= NADPH_binding_site
                                                                                     .63. .164
'label= NADPH_binding_site
                                                                                                                  234. .241
|label= NADPH_binding_site
136. .237
|label= FAD_binding_site
                                                                                                           label= NADPH_binding_site
NADPH_binding_site
            NADPH_binding_site
                                                                                                                                                                                         75. .295 _
|abel= FAD_binding_site
                                                                                                                                             40. 249
|abel= FAD_binding_site
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        .31. .143
'label= NA
                                           .151
                      35, 138
'label=
                                           148.
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                     Disulfide-bond
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06-APR-2000; 2000US-0195055P.

(PHAA ) PHARMACIA & UPJOHN CO

Benson TE;

WPI; 2002-034237/04.

Crystallizing Staphylococcus aureus thioredoxin reductase molecule or molecular complex by preparing purified thioredoxin reductase and crystallizing from solution comprising dimethyl sulfoxide and sodium formate.

Claim 52; Fig 11; 147pp; English.

The present sequence is that of a recombinant Staphylococcus aureus thioredoxin reductase (TrxB) the crystal structure of which is solved in the specification. Thioredoxin reductase is a two domain protein composed of a flavin adenine dinucleotide (FAD) binding domain and a reduced betanicoctinamide adenine dinucleotide phosphate (NADPH) binding domain. The specification describes the crystallisation of S. aureus thioredoxin be used to design an inhibitor complex. The crystal of the invention may be used to design an inhibitor of S. aureus thioredoxin reductase molecule or molecular complex. The crystallising a S. aureus thioredoxin for solving the structure of other molecules or molecules of the complexes and designing inhibitors of S. aureus thioredoxin reductase. A composition compressing the inhibitors is useful for preventing and treating S. aureus thioredoxin reductase mediated disease

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New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.
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                                                                                                                                                                        180
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                                                                                                                                         121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGFFTKFADKVTIVHRRDEL 180
                                                                                                                                                                                                                                                                                 Thioredoxin reductase; TrxB; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis.
                                                                                                                                                                                                                    RAQRILQDRAFKNDKIDFINSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG
                                                                                                                                                                                                                                        181 KAQRILQDRAFKUDKIDFIWSHTIKSINEKDGKVGSVTLTSIKDGSEETHEADGVFIXIG
                                                                                                                        GPDLSTKMPEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG
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                                                                         1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT
                                                                                         Gaps
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                           Length 320;
                                                    Indels
                     Score 1662; DB 5;
Pred. No. 3e-146;
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/label= Antigenic_epitope
210. .212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. aureus thioredoxin reductase, TrxB
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                              100.0%; Sc
100.0%; Pr
ive 0;
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                                              Best Local Similarity 100.
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-183259/18.
N-PSDB; AAS00915.
                                             Similarity
        Sequence 320 AA;
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Staphylococcus infections. The polypeptides of the invention are used to detect anti-Staphylococcus antibodies in a biological sample from an canimal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genus and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection, callulitis, burn infection, evelid infection, food poisoning, confiction, neonatal conjunctivitis, osteomyelitis, skin infection, disease and Lyell's disease, toxic epidermal necrosis, Ritter's cold-sease and Lyell's disease, toxic shock syndrome and endocarditis. The polymucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods
                                                                               The sequence represents S. aureus TrxB (Thioredoxin reductase). The polymuclectides of the invention are used to detect Staphylococcus nucleic acids in a biological sample from an animal for diagnosing
                               9; Page 16; 225pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 AA;
                            Claim
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GPDLSTKWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
                                                                                                                                      GPDLSTRMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVITATGAEYKKIG 120
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                                                        MGTEIDFDIALIGAGPAGWTAAVYASRANLKTVMIERGIPGGQWANTEEVENFPGFEMIT
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                                                                                                                                                                                                                                  SEETHEADGVFIYIG
                                                                                                                                                                                                                                                                                     MTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS
                                      0;
           Length 312;
                                    2; Indels
                                                                                                                                                                   VPGEQELGGRGVSYCAVCDGAFFKNKRLFV1GGGDSAVEEGT
                                                                                                                                                                                                                        RAQRILQDRAFKNDKIDFIWS#TTKS|NEKDGKVGSVTLTST
                                                                                                                                                                                              VPGEQELGGRGVSYCAVCDGAFFREKRLFVIGGGDSAVEEG
       Score 1593; DB 4;
Pred. No. 7.7e-140;
                                 0; Mismatches
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Query Match

Best Local Similarity 99.4%;
Matches 310; Conservative
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(first entry)
                                 Staphylococcus aureus
                                     WO200294868-A2.
              20-NOV-2003
         ABM72250
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RESULT 3

27-MAR-2002; 2002WO-1B002637.

28-NOV-2002.

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Sequence 311 AA;
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                                                                                                                                                                                                                                                                                                                     gene therapy; infection; sepsis; diagnosis;
                                                                                                                                                                                                                                                                                                 Staphylococcus aureus protein #1490.
                                                                                                                                                                                                                                           ABM72250 standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                   Antibacterial; vaccine; gene therar
enzymatic assay; antibiotic target
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protein, useful as a vaccine for treating or infection, specifically an infection caused by
                                                                                                                                                                                                                                                                         The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSTKWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism; antibacterial; neuroprotective; immunosuppressive; antiinflammatory; antiulcer; immunostimulant; ophthalmological; pathogenic microbe; bacteraemia; septic shock; organ infection; skin infection; bacterial basal colonisation; bacterial eye infection; septicaemia; tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEQELGGRGVSYCAVCDGAFFKNKRLFV1GGGDSAVEEGTFTTKFADKYTIVHRRDELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFFMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHEADGVFIYIGMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 QRILQDRAFKNDKIDFIWSHTLKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1582; DB 6;
Pred. No. 8.1e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus antigenic protein #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2980; 49pp; English.
                                                                              Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA89500 standard; protein; 309 AA.
     27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.2%;
                                                                                                                                                                       aureus
                                                                                                                                                                                        preventing Staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.40
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                      S. aureus, e.g. sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYIEHLNDQA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYIEHLNDOA 311
                                                                              Mora M,
                                                                                                             WPI; 2003-120786/11.
                                                                                                                                                                   New Staphylococcus
                                    (CHIR-) CHIRON SPA
                                                                                                                                N-PSDB; ACF73810
                                                                           Masignani V,
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62 61 182

242 181

121

us-09-825-212-1.rag

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The present invention describes an antigenic protein or its part, which is for use as a vaccine. The antigenic protein is encoded by an isolated by a patholococcus aureus or S. epidermidis partial gene but a patholococcus aureus or S. epidermidis partial gene composition comprising at least one antigenic protein; (2) and which encodes a protein expressed by a pathogenic organism. Also described: (1) a vaccine composition comprising at least one antigenic protein; (2) a method of composition animal against a disease or condition caused by a pathogenic microbe by administering the antigenic protein or the vaccine; pathogenic microbe by administering the antigenic protein or the vaccine; (3) an antibody or its binding part obtainable by the method above; (4) composition at produced by the method of (4); and (6) identifying opsonic antigens expressed by a pathogenic microbe. (5) a hybridoma cell line produced by the method of (4); and (6) identifying opsonic antigens have antibacterial, menroprotective, immunosuppressive, antiinflammatory, antiulcer, immunostimulant and ophthalmological criticial and can be used for immunisting an animal (specifically a human) against a disease or condition caused by a pathogenic microbe, e.g. capinst a disease or condition caused by a pathogenic microbe, e.g. capinst a disease or condition caused by a pathogenic microbe, e.g. capinst a colonisation, bacterial eye infections, skin infections, bacterial condition caused by a pathogenic microbe, e.g. cateritis, sepsis, meningitis, pneumonia, stomach ulcers, ganorinose, cateritis, impetigo, histoplasmosis, lyme disease, gastro-enteritis, dysentery, shigellosis, S. aureus-associated septicemia, peritonitis or sakin disorders, S. epidermidis-associated septicemia, peritorionic peritorionic peritorionic peritorionic peritorionic pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLSTRWFEHAKKFGAVYQYGDİKSVEDKGEYKVINFGNKELTAKAVITATGAEYKKIGVP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic polypeptides from Staphylococcus aureus or S. epidermidis, useful as a vaccine for immunizing humans against e.g. bacteremia, septic shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEIDFDIAIIGAGPAGWTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMITGP
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sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock; necrotising fasciitis; impetigo; histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a S. aureus antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Brummel K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.6%; Score 1573; DB 6; 99,4%; Pred. No. 5.6e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcdowell P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 131; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Clarke S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 99,4%;
306; Conservative
                                                                                                                                                                                                                                                                                               02-AUG-2001; 2001GB-00018825
09-JAN-2002; 2002GB-00000349
                                                                                                                                                                                                                                                02-AUG-2002; 2002WO-GB003606
                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                   (UYSH-) UNIV SHEFFIELD
                                                                                                         Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-256434/25
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mond J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 309 AA;
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Best Local S:
Matches 306
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                                                                                                                                                                                                                                                                                                                                                                                            (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                         242
                                                 241
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                                                                                       242 PLTAPFKDLGIINDVGXIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 301
122 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFLTKFADKVTIVHRRDELRA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents Staphylococcus thioredoxin reductase (TrxB). TrxB inhibitors can be used as antimicrobials to treat a Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are antimicrobials to which, unlike most of those in the prior art, Staphylococcus has not yet developed a resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TEIDEDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DLSTRMFEHARKFGAVYQYGDIKSVEDKGEYKVINFGNKELTARAVITATGAGYKKIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEQELGGRGYSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 İBİDEDİAİİGAĞBAĞMTAAVYASRANLKIVMIERGIPGGQMANTEEVENFPGFEMITGP
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                                         PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                         QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK
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                                                                                                                                                                                                                                                                                              Staphylococcus aureus trxB open reading frame protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 311;
                                                                                                                                                                                                                                                                                                                      Staphylococcus; trxB; thioredoxin reductase; antimicrobial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new thioredoxin reductase from Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1561; DB 2;
Pred. No. 7.4e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uziel O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ö
                                                                                                                                                                                                                         AAY29854 standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.9%;
ilarity 98.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US004512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0076525P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borovok I,
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                   EYIEHLND 310
                                                                                                                                                          302 EYİEHLND 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aharonowitz Y,
                                                                                                                                                                                                                                                                                                                                                                                WO9945123-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304;
                                                                                                                                                                                                                                                                              17-NOV-1999
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                                                                                                                                                                                                                                                     AAY29854;
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                                                                                   243
                                  183
                                                                                                                                      303
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                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                   AAY29854
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(gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to ABP60964 represent sequence given in the exemplification of the present

Sequence 311 AA;

invention

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Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic; vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer; food product; milk; wheat; oxidative stress; cateract; diabetes; chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing oil body associated with recombinant multimeric protein comple e.g. redox proteins and immunoglobulins comprises producing recombinant polypeptides capable of forming the complex in cells comprising oil bodies.
                                 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dalmia BK;
                                                                                                                                                                                                                            Staphylococcus aureus thioredoxin reductase SEQ ID NO:265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Briggs SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heifetz PB,
Moloney M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 82; Page 315-316; 362pp; English.
                                                                                                                                                        ABP60916 standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SEMB-) SEMBIOSYS GENETICS INC. (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                   disease
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000; 2000US-00742900.
05-JUL-2001; 2001US-0302885P.
04-DEC-2001; 2001US-00006038.
                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001WO-US050240
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                gastro oesophageal reflux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G, Deckers F
Zaplachinski
                                                                             EYIEHLNDQA 312
                                                                                                  GYIEHLNDOA 311
                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-508806/54.
                                                                                                                                                                                                                                                                                                                                                                           WO200250289-A1
                                                                                                                                                                                                      06-SEP-2002
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            182
                                                                             303
                                  243
                                                                                                                                                                                 ABP60916;
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                                                                                         DISTRMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                           242
                                                                                                            DESTRUFEHARKFGAVYQYGDIKSVEDKGEYKVINFGNKELTARAVITATGAGYKKIGVP 121
                                                                                                                                      GEOELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                      PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                    62
                                                                                                                                                                                                                                              61
                                           3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                2 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                                                                   QRILODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK
                                                                                                                                                                                                 The present sequence represents Staphylococcus thioredoxin reductase (TrxB). TrxB inhibitors can be used as antimicrobials to treat a Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are antimicrobials to which, unlike most of those in the prior art, Staphylococcus has not yet developed a resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis trxB open reading frame protein seguence.
                             .,
    Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus; trxB; thioredoxin reductase; antimicrobial
                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new thioredoxin reductase from Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katz
  Score 1561; DB 5;
Pred. No. 7.4e-137;
                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uziel O,
                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                                                                                            AAY29855 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 7; 59pp; English.
 93.9%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US004512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0076525P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                312
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                                                                                                                                                                                                                                                                            303 EYIEHLNDQA
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            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ21081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aharonowitz Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9945123-A1.
                     Matches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-1999;
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                                                                                          63
                                                                                                                                       123
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Query Match
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The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). MI comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (Pl. P2), where Pl is capable of associating with CC p2 to form the MPC and associating the complex with an occlusion body CC p1. M1 is useful for producing an oil body associating with OB and CC MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care CC product which reduces the oxidative stress on the surface area of the cumman body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, cused to treat chronic obstructive pulmonary disease, psoriasis, cataracts, callidates, reperfusion injury, wound healing, sepsis, gastro contestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD

us-09-825-212-1.rag

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19-DEC-2001; 2001WO-US050240.
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06-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the
                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                               PLIAPFKDLGIINDVGYIVTKDDMTISVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                   122
                                                                                                                     121
                                                                                                                                        182
                                                                                                                                                    242
                                                                                                                                                                                       19
                                                               3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGP
                                                                                                   DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP
                                                                                                             GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                            QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHBADGVFIYIGMK
                                                                              TEVDFDVAIIGAGPAGMTAAVYASRANLKTVMIERGMPGGOMANTEEVENFPGFEMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                           S. epidermidis open reading frame protein sequence SEQ ID NO:1142.
                                               .
0
                             Length 310;
                                              Indels
                                                 13
                           Query Match
Best Local Similarity 90.3%; Pred. No. 5.6e-127;
Matches 278; Conservative 17; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 330; 2188pp; English.
                                                                                                                                                                                                                                                                                                                       AAG82024 standard; protein; 310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000; 2000WO-US030782
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                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis.
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DXITELKD 309
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N-PSDB; AAH52874.
            Sequence 310 AA;
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polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.

The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the control of S. epidermidis infections. e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 complification of the present invention. N.B. The present invention exemplification of the present invention. N.B. The present invention sequence listing of the present specification, however the sequence is sequence listing of the present specification, however the sequence is listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present in the constant of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the present specification of the sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%; Score 1455; DB 4; Length 3: 90.3%; Pred. No. 5.6e-127; ive 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillis subtilis thioredoxin reductase SEQ ID NO:198.
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Best Local Similarity 90.31
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 310 AA;
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Heifetz PB,
Moloney M;
                                                                                                      Claim 82; Page 268-269; 362pp; English.
                             (SEMB-) SEMBIOSYS GENETICS INC. (SYGN ) SYNGENTA PARTICIPATIONS AG.
       19-DEC-2000; 2000US-00742900.
05-JUL-2001; 2001US-0302885P.
04-DEC-2001; 2001US-00006038.
                                              Rooijen G, Deckers H,
Val G, Zaplachinski S,
                                                               WPI; 2002-508806/54
      19-DEC-2000;
                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                            ABP60964
                                               Van
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Sequence 315 AA;

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7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                                              KMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE
                                                                                          KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                                                      127 LGGRGYSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
                             Gaps
                            0;
    Length 315;
                          55; Indels
69.4%; Score 1154; DB 5; 71.4%; Pred. No. 6.5e-99;
             ; Pred. No. 6.5e
33; Mismatches
                  datches 220; Conservative
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        Local Similarity
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Query Match
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AAO20618 standard; protein; 315 AA.

AAO20618 ID AAO2

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The present invention describes a method (MI) for producing an oil body associated with a recombinant multimeric protein complex (MPC). MI comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (PI, P2), where PI is capable of associating with CP2 to form the MPC and associating the complex with an occlusion body CP3 to form the MPC and associating the complex with an occlusion body CP1 MI is useful for producing a noil body associating with OB and MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care broader the oxidative stress on the surface area of the used to recat chronic obstructive pulmonary disease (COPD), cataracts, disabetes, envenomation, bronchiopulmonary disease (COPD), cataracts, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GID), ulcers, GERD
                                                                                                                                                                                      complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to ABP60964 represent sequence given in the exemplification of the present invention. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 QARAFDNEKVDFLMNKTVKEIHEENGKVGNVTLVDTVTGEESBFKTDGVFIYIGMLPLSK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 PFKDLGITNDVGYIVTKDDMTTSVPGIPAAGDVRDKGIRQIVTATGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFENLGITNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDGSIAAQSVQHYVE 305
                                                                                                                                                                          Producing oil body associated with recombinant multimeric protein comple
e.g. redox proteins and immunoglobulins comprises producing recombinant
polypeptides capable of forming the complex in cells comprising oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                             Dalmia BK;
                                                                                                           Briggs SP,
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Ophthalmological; virucide; vulnerary; vasotropic; antiallergic; cofactor specificity; thioredoxin reductase; TR; non-allergenic food; computational mutagenesis; scaffold protein; oil body; animal feed; digestibility; gluten; protein disulfide isomerase; PDI; enzyme; scleroprotein; gelled; food; nitrosative stress response; eye disease; cataract; oxidative stress; ischemic-reperfusion; acute lung injury.
                                                                                                                                                              Thioredoxin reductase variant protein sequence #17.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                 10-APR-2003
AAO20618;
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WO200290300-A2

14-NOV-2002

Desjarlais JR, Heifetz SYGN ) SYNGENTA PARTICIPATIONS AG. Del Val G, 06-MAY-2002; 2002WO-US014358 04-MAY-2001; 2001US-0289029P. 05-APR-2002; 2002US-0370609P. 29-APR-2002; 2002US-00370609. P, Muchhal U; Dalmia BK, WPI; 2003-111951/10. XENCOR Briggs SP, Luginbuhl E (XENC-)

Altering cofactor specificity of target protein, e.g. thioredoxin reductase, useful for reducing antigenicity of glutens in wheat, barley, or treating disulfide linkages present in proteins, by computational mutagenesis

Disclosure; Fig 21B; 212pp; English.

The invention relates to a novel method for altering the cofactor specificity of a target protein (e.g. thioredoxin reductase (TR)) by computational mutagenesis. This method involves inputting a set of condinates for a scaffold protein comprising amino acid positions, applying at least one protein design cycle, and generating a set of candidate variant proteins with altered cycle; and generating a set of method is useful for altering the cofactor specificity. The novel proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces, Neurospora crassa, Arabidopeis, and human. Another compared of the invention is useful for making oil bodies which are useful in the preparation of non-allergenic foods, or in the preparation of protein is useful for reducing the antigenicity of glutens in wheat, rye command is useful for reducing the antigenicity of glutens in wheat, rye contains useful for reducing the antigenicity of glutens in wheat, rye including a number of plant and mammalian proteins found to contain thoreases, etc; and structural proteins such as scleroproteins.

Compositions comprising variant TR proteins such as scleroproteins.

Compositions comprising variant TR proteins and PDI are useful for reating protein disulfide crosslinks yielding plants expressing variant compositions, and thus is useful in food processing. A further compositions, and thus is useful in food processing. A further compositions composition is useful for producing plants expressing variant of TR protein, e.g., corn and soybean provides grains with altered storage. The mormal grain during industrial processing or animal dispersion of variant ry protein quality as well as grains that perform quality is a variant province in the processing or animal variant province in the province in the processing or animal variant province in the processing or animal variant province in the processing or animal variant province in the processing or animal variant province in the processing or animal variant province in variant TR proceins in combination with thioredoxin, which can used to manipulate nitrosative stress, to upregulate nitrosative stress responses, and thus is useful for treating eye diseases, such as catearacts, where it inhibits or reverse formation of cataract in eye. The variant TR protein in combination with thioredoxin is also useful for minimizing oxidative stress and ischemic-reperfusion induced in acute invention relates to a novel method for altering the cofactor

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RESULT 12
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                                                                                                                                                                                            PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
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                                                                                                                                                              ODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                    9
                                                                                                                                LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFŢTKFADKVTIVHRRDELRAQRIL
                                                                                                                                                                        7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                                                               KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                             66 XMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE
                                                                                                                                        lung injury. This sequence represents a thioredoxin reductase variant protein of the invention
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                         Thioredoxin reductase; TRR; cofactor specificity; computational mutagenesis; substrate specificity; PDA; protein design automation; toxic protein; food allergenicity; food digestibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heifetz P;
                                         Length 315;
                                                        Indels
                                                          55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desjarlais JR,
                                         69.4%; Score 1154; DB 6; 71.4%; Pred. No. 6.5e-99;
                                                        33; Mismatches
                                                                                                                                                                                                                                                                                ADD26553 standard; protein; 315 AA.
                                                                                                                                                                                                                                                                                                                             B. subtilis thioredoxin reductase.
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05-APR-2002; 2002US-0370609P.
29-APR-2002; 2002US-0376682P.
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                                                                                                                                                                                                                                                                                                               15-JAN-2004 (first entry)
                                          Query Match
Best Local Similarity 71.48
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brigge SP, ' Muchhal U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESJARLAIS J R.
                                                                                                                                                                                                                             307 HLNDQARS 314
                                                                                                                                                                                                                                            ELQETLKT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEIFETZ P.
LUGINBUHL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-801212/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALMIA B K.
BRIGGS S P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUCHHAL U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAL G D.
                                                                                                                                                                                                                                                                                                                                                                                                 US2003100743-A1.
                             Sequence 315 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2003
                                                                                                                                                                                                                                                                                                 ADD26553;
                                                                                                                                                                                                                                                                                                                                                                                   Bacillus
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(BRIG/)
(VALG/)
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The invention relates to altering the cofactor specificity of thioredoxin candidates (TRR) comprising computational mutagenesis. Also included are reductase (TRR) comprising computational mutagenesis. Also included are a tearget protein, a variant TRR protein that reduces a protein that reduces a thioredoxin protein (charies subtiles, Mycobacterium leprae, Saccharomyces, Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces, CC Neurospora crasas, Arabidopsis, and human), a variant TRR protein, that is either a wild-type TRR protein, thioredoxin, or a variant TRR protein, producing a plant with a modified TRR protein, or a transformed plant prepared by the method and a transformed seed of the ctransformed plant. The cofactor specificity of the variant TRR is altered to that the variant preferentially binds NADPH compared to NADH, or such that the variant preferentially binds NADPH compared to NADH, or vice versa. The protein design cycle comprises protein design automation or a force field calculation. The variant TRR protein is fused to the second protein through a linker. The variant TRR protein has 1.3 amino caid substitutions are selected from positions A4, A5 and A6, The amino acid substitutions are selected from positions A4, A5 and A6, preferably from RA4W, RA5L, RA5W, RA5I, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y, RA5Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
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Altering the cofactor specificity of thioredoxin reductase, useful for reducing the toxicity of toxic proteins, reducing allergenicity of food and increasing the digestibility of foods, comprises computational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFKDLGITNDVGY1VTKDDMTTSVPG1FAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE
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                                                                                                                                                                                                                 Disclosure; Fig 21; 125pp; English
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Best Local Similarity 71.4
Matches 220; Conservative
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cofactor specificity; thioredoxin reductase; TR; non-allergenic food; computational mutagenesis; scaffold protein; oil body; animal feed; digestibility; gluten; protein disulfide isomerase; PDI; enzyme; scleroprotein; gelled; food; nitrosative stress response; eye disease; cataract; oxidative stress; isohemic-reperfusion; acute lung injury. vulnerary; vasotropic; antiallergic; virucide; Ophthalmological;

Unidentified

WO200290300-A2

14-NOV-2002

06-MAY-2002; 2002WO-US014358

04-MAY-2001; 2001US-0289029P. 05-APR-2002; 2002US-0370609P. 29-APR-2002; 2002US-00370609.

(SYGN ) SYNGENTA PARTICIPATIONS AG (XENC-) XENCOR

Heifetz P; Desjarlais JR, <u>ن</u> Val Del Dalmia Luginbuhl P, Briggs SP,

WPI; 2003-111951/10

barley, Altering cofactor specificity of target protein, e.g. thioredoxin reductase, useful for reducing antigenicity of glutens in wheat, bar] or treating disulfide linkages present in proteins, by computational

Disclosure; Fig 22; 212pp; English.

The invention relates to a novel method for altering the cofactor specificity of a target protein (e.g. thioredoxin reductase (TR)) by computational mutagenesis. This method involves inputting a set of computational mutagenesis. This method involves inputting a set of condutational mutagenesis. This method involves inputting a set of captor specificity at least one protein design cycle; and generating a set of candidate variant proteins with altered cofactor specificity. The novel proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium ethod is useful for Escherichia coli, Bacillus subtilis, Mycobacterium sethod of the invention is useful for making oil bodies which are useful in the preparation of non-allergenic foods, or in the preparation of non-allergenic foods, or in the preparation of non-allergenic foods, or in the preparation of non-allergenic foods, or in the preparation of non-allergenic foods, or in the preparation of protein is useful for reducing the antigenicity of glutens in wheat, ryce or barley, to reduce alternative substrates for thioredoxin reductases, including a number of plant and mammalian proteins found to contain. The protein is useful as a redox partner in compositions used for treating damplases, etc; and structural proteins such as sclaroproteins. Compositions, and thus is such as sclaroproteins. Compositions, and thus is useful for producing plants expressing variant compositions, and thus is useful in food processing. A further composition, e.g., corn and soybean provides grains with alteriatively differently responses, and thus is useful for producing plants expressing variant or protein quality as well as grains that perform qualitatively differently variant TR proteins in combination with thioredoxin, which can used to responses, and thus is useful for treating eye diseases, such as useful for reating eye diseases, such as useful for reating eye diseases, such as a caraacts, where it inhibits or reverse formation of cataracts in eventse formation with thioredoxi variant TR protein in combination with thioredoxin is also useful for minimizing oxidative stress and ischemic-reperfusion induced in acute This sequence represents a thioredoxin reductase variant lung injury. This sequenc protein of the invention

Sequence 315 AA;

Query Match

DB 6; Length 315; Score 1152; 69.3%;

0 126 KMFEHAKKEGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE 125 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186 LGGRGVSYCAVCDGAFFKGKELVVVGGGDSAVEEGVYLTRFASKVTIVHRRDKLRAQSIL 185 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246 306 99 65 KWFBHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST 6 YDVIIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILGPELSN PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE Gaps . 55; le-98; Mismatches Pred. No. 34, 71.18; Conservative 306 ELQETLKT 313 HLNDQARS 314 Best Local Similarity 219; 67 127 126 187 247 307 Matches q ò g ò 8 ð qq ð g ò g

RESULT 13

ABP60886 standard; protein; 315 AA **AB**P60886

ABP60886;

(first entry) 06-SEP-2002

Bacillus halodurans thioredoxin reductase SEQ ID NO:235.

Multimeric protein, redox protein, thioredoxin, thioredoxin reductase; oil body, ophthalmological, antidiabetic; cytostatic; antipsoriatic; vasotropic, vulnerary; antibacterial; immunosuppressive, antiulcer; food product, milk; wheat; oxidative stress; cataract; diabetes; catoronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer; gastro oesophageal reflux disease.

Bacillus halodurans

WO200250289-A1.

27-JUN-2002

19-DEC-2001; 2001WO-US050240.

19-DEC-2000; 2000US-00742900. 05-JUL-2001; 2001US-0302885P. 04-DEC-2001; 2001US-00006038. 19-DEC-2000; 05-JUL-2001;

SYGN \ SYNGENTA PARTICIPATIONS AG SEMB-) SEMBIOSYS GENETICS

Briggs SP, Dalmia BK; Heifetz PB, Moloney M; Van Rooijen G, Deckers H, Del Val G, Zaplachinski S,

WPI; 2002-508806/54.

Producing oil body associated with recombinant multimeric protein complex e.g. redox proteins and immunoglobulins comprises producing recombinant polypeptides capable of forming the complex in cells comprising oil

Claim 82; Page 296-297; 362pp; English.

for

Heifetz

Desjarlais JR,

Val GD,

Dalmia BK, Briggs SP, \ Luginbuhl P, Muchhal U;

WPI; 2003-801212/75.

DESJARLAIS J R HEIFETZ P. LUGINBUHL P. DALMIA B K. BRIGGS S P. VAL G D.

(DALM/) (BRIG/) (VALG/) (DESJ/)

MUCHHAL U.

MUCH/) (HEIF/) LUGI/)

04-MAY-2001; 2001US-0289029P. 05-APR-2002; 2002US-0370609P. 29-APR-2002; 2002US-0376682P.

06-MAY-2002; 2002US-00141531

Altering the cofactor specificity of thioredoxin reductase, useful reducing the toxicity of toxic proteins, reducing allergenicity of and increasing the digestibility of foods, comprises computational

Claim 30; Page; 125pp; English.

mutagenesis.

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The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with CC recombinant polypeptide (P1, P2), where P1 is capable of associating with a second complex with an occlusion body CC (OB) through an OB-targeting-protein capable of associating with OB and CC (DB) through an OB-targeting-protein capable of associating with OB and CC MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care command to be compacted as a first capable of association of the composition of the composition of the composition of the composition of the composition of diabetes, envenomation, bronchiopulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease (COPD), cataracts, call and composition of intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (Gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to intestinal experience given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GMLPINEAVKNINIINDEGYIVTNEEMETSVPGIFAAGDVREKSLRQIVTATGDGSLAAQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGPELSTKMFEHAKKFGAEYAYGDIKEIIDQGDLKLVKAGNKEYKARAVIVATGAEYKKI 120
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 315;
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                 68.9%; Score 1145.5; DB 68.6%; Pred. No. 4.1e-98; tive 38; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD26570 standard; protein; 309 AA.
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Best Local Similarity 68.6%
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 315 AA;
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The invention relates to altering the cofactor specificity of thioredoxin conductase (TRR) comprising computational mutagenesis. Also included are reductase protein, a variant TRR protein that reduces a protein that reduces a thioredoxin protein (obtained from an organism selected from a thioredoxin protein (obtained from an organism selected from Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharowyces, CC assord protein (that is either a wild-type TRR protein, thioredoxin, or a variant TRR protein, producing a plant with a modified TRR protein, therefore a transformed plant. The offactor specificity of the variant TRR is altered contransformed plant. The offactor specificity of the variant TRR is altered couch that the variant preferentially binds NADPH compared to NADH, or vice versa. The protein design cycle comprises protein design algorithm, or a force field calculation. The variant TRR protein also the cord substitutions as compared to the wild-type Arabidopsis TR protein. The variant TRR protein has 1-3 amino caid substitutions are selected from positions A4, A5 and A6, preferably from RA4W, RA51, RASM, RA51, RA57, RA57, RA59, RA67, RA69, and RA6N. The method is useful for reducing the toxicity of toxic proteins, reducing allergenicity of food and increasing the coxicity of toxic proteins, reducing allergenicity of food and increasing the coxicity of the method as compared to prior art. The present sequence is a synthetic continuation. The versent sequence is a synthetic continuation.
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Matches 214; Conservative
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Synthetic

29-MAY-2003

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PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
                                     ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP33124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can particularly S. epidermidis infections. The sequences can particularly S. epidermidis infections. The sequences can be used to or inhibit S. epidermidis infections. The sequence can be used to or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5512; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                           ABP40667 standard; protein; 253 AA.
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97US-0064964P.
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N-PSDB; ABN93212.
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08-NOV-1997;
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LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246

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129 QERAFKNDKVDFIWSHTLKTINEKDGKVGSVTLESTKDGAEQTYDADGVFIYIGMKPLTA 188
                           247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
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(c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein -

September 15, 2004, 12:13:58 Run on:

8 ; Search time 40 Seconds (without alignments)

(without alignments)
769.532 Million cell updates/sec

US-09-825-212-1

Perfect score:

1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH Sequence:

320

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* 1 C1 F6 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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ваувау thioredoxine reductase [imported] - Staphylococcus aureus (strain N315)

Cibate: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
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Rikuroda, M.; Ohta, T.; Tohiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Cipate: A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89849
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Gaps 0 Length 311; Indels Score 1582; DB 2; Pred. No. 2.9e-111; 0; Mismatches 2; Query Match
Best Local Similarity 99.4%;
Matches 308; Conservative

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62 61 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP 2 TEIDFDIAIIGAGFAGMTAAVYASRANLKTVMIERGIPGGGMANTEEVENFPGFEMITGP 셤 à

122 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 63 62 ò d

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182 181 123 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA à d

242 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 183 g ò

241 302 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 182 ( 243 ò

301

EYIEHLNDOA 312 FYIEHLNDQA 311 303 302 ò

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N RESULT

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C;Accession: C84096
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Recference number: A83650; MUD:20512582; PMID:11058132
A;Accession: C84096
A;Accession: C84096
A;Assaidus: preliminary
A;Molecule type: DNA
A;Mosidus: preliminary
A;Molecule type: STTO-
A;Residus: 1-315 <STO-
A;Csors-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07290.1; GSPDB:GN00
A;Experimental source: strain C-125
G;Genetics:
A;Gene: tras
C;Genetics:
A;Gene: tras
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGTEID-PDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.9%; Score 1145.5; DB 2; 68.6%; Pred. No. 1.6e-78; ive 38; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315
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Best Local Similarity 65.8
Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 68.6
Matches 216; Conservative
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C; Accession: A69727

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter R; Kunst, F.; Ogasawara, N.; Entsian, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Che A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masudel, S.; Maucell, M.; Frivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, V.; Tamakoshi, A.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, T.; Tanaka, M.; Tanaka, T.; Tanaka, M.; Tanaka, T.; Tanaka, M.; Tanaka, T.; Tanaka, M.; Tanaka, T.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tanaka, M.; Tan
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A, Residues: 1-316 < KUN>
A, Residues: 1-316 < KUN>
A, Residues: 1-316 < KUN>
A, Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15484.1; PID:g2635992
A, Experimental source: strain 168
C; Genetics:
A, Genetics: A, Genetics: C; Genetics: death of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of control of the condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of condition of
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                                                                                                                     C;Species: Bacillus subtilis
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
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                                                                    thioredoxin-disulfide reductase (EC 1.8.1.9) - Bacillus subtilis
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Matches 222; Conservative
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Listeria innocua (strain Clip11262)

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C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 1057; DB 2; Length 319; 65.8%; Pred. No. 7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL592022; PIDN:CAC97848.1; PID:g16415158; A;Experimental source: strain Clip11262
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C. Accession: D86742
R. Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
A./Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s. A./Recession: D86742
A./Accession: D86742
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-308 <STO>
A./Cross-references: GB:AE005176; PID:g12723876; PIDN:AAK05038.1; GSPDB:GN00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Streptococcus pneumoniae (stra
                                                                                                                                                 subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cypedaxin disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae Cispecies: Streptococcus pneumoniae Cispecies: Streptococcus pneumoniae Cispecies: Streptococcus pneumoniae Cispecies: 22-Oct-2001 #text_change 03-Jun-2002 Ciscession: G98032 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002 Riffocies: 03-M. J. A. Aborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeBOfff, B.; F. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, B. Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 201
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, Brumoniae Strain R6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE007317; PIDN:AAL00116.1; PID:g15458956; GSPDB:GN00174
                                                                                                                                    thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Lactococcus lactis
C.Species: Lactococcus lactis subsp. lactis
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TEKKYDVVIIGSGPAGMTAAMYTARSEMKTLLLERGVPGGQMNTAEIENYPGYETIMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 QEIIQQRAFKEEKINFIWDSVPMEIKGDDKKVQSVVYKNVKTGEVTEKAFGGIFIYVGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.5%; Score 872; DB 2; 53.1%; Pred. No. 5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain IL1403
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KFVAELD 308
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-303 < KUR>
                                    ELKE 311
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hes 163;
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Best Local S:
Matches 163
                                    308
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thioredoxin reductase [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Becies: Listeria monocytogenes
C;Accession: AF1384
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C;Accession: AF1384
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D; Doninguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madueno, E.; Maitournam, A.; Mayauthors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species
A;Title: Comparative genomics of Listeria species
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Ccession: AF1384
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Ccession: AF1384
A;Ccession: AF1384
A;Cross-references: GB:MC 003210; PIDN:CAD00556.1; PID:g16411966; GSPDB:GN00177
C;Genetics:
A;Gene: trxB
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                             KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 126
                                                                                           LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
                                                                                                                                                                        QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                       PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                  248 AFLSLGITDEEGYIVTDEEMRINLPGIFAAGDVRAKSLRQIVTATGDGGLAGQNAQKYVE 307
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7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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65.5%; Pred. No. 1.2e-71;
ive 43; Mismatches 62;
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Matches 199; Conser
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J.D.; Dodson, R.J.;
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residuae: 1-325 < WHI>
A,Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11534.1; PID:g645977
A,Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
CiAccession: AF330
Cispecies: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
Cibacession: AF30
Cispecies: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEXI- 305
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A;Map position: 1
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
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48.4%; Pred. No. 3.1e-47;
tive 51; Mismatches 100;
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Best Local Similarity 48.4
Matches 152; Conservative
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C;Species: Streptococcus pneumoniae
C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: 055169
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Refearence number: A95000; MUID:21357209; PMID:11463916
A;Recession: G95169
A;Status: preliminary
A;Wolceule type: DNA
A;Residues: 1-303 <a href="https://docume.com/drafts/">https://docume.com/drafts/</a>
A;Cross-references: GB:AE005672; PIDN:AAK75552.1; PID:g14972947; GSPDB:GN00164; TIGR:SP4
A;Residues: 1-303 <a href="https://docume.com/drafts/">https://docume.com/drafts/</a>
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KMFEPLENLGVEHIXGYVENVEDHGDFKKVMTDDQTYETRTVIVATGSKHRPLGVPGEEE
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                                                                                                                                                                                                                                                                     7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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C;Superfamily: thioredoxin reductase, thioredoxin reductase homology
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                               A,Gene: trxB
C,Superfamily: thioredoxin reductase, thioredoxin reductase homology
C,Keywords: oxidoreductase
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                                                                                                                                       Query Match 51.2%; Score 851; DB 2; Length 303; Best Local Similarity 54.0%; Pred. No. 1.9e-56; Matches 163; Conservative 55; Mismatches 82; Indels
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Best Local Similarity 53.6%; Pred. No. 2.6e-56; Matches 162; Conservative 57; Mismatches 81
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A; Reference number: S38988; MUID:9403119; PMID:8223622
A; Residues 1.318 988
A; Molecule type: DNA
A; Residues 1.315 c.ULE>
A; Accssion: S38988; MUID:9403119; PMID:8223622
A; Molecule type: DNA
A; Residues 1.1315 c.ULE>
A; Cross-references: GB:104500; NID:g2708733
B; Dietrichs, D: Meyer, M.; Schmidt, B.; Andreesen, J.R.
A; Cross-references: GB:10450; NID:92708733
B; Dietrichs, D: Meyer, M.; Schmidt, B.; Andreesen, J.R.
A; Molecule type: Drothin C NADPH-dependent electron-transferring flavoproteins and N-termin A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Molecule type: protein
A; Residues: 1-33, X, 35-46, X, 48, 'D', 50-55 c.DIE>
A; Molecule type: protein
A; Residues: 1-33, X, 35-46, X, 48, 'D', 50-55 c.DIE>
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Complex: homodimer; each chain has a tightly associated but noncovalently bound PAD
A; Bastr codon:
C; Function:
C; Function:
C; Superfamily: thioredoxin reductase; thioredoxin reductase homology crack of S; Superfamily: thioredoxin reductase; hinoredoxin reductase homology crack of S; Superfamily: thioredoxin reductase; homodimer; near-alpha-beta PAD nucleotide-binding fold
F; 1-309/Domain: thioredoxin reductase homology crack firstus predicted
F; 1-309/Domain: thioredoxin reductase homology crack firstus predicted
F; 134-137/Disulfide bonds: redox-active #status predicted
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Eur. J. Blochem. 234, 192-199, 1995
A:Title: Glycine reductase of Clostridium litorale. Cloning, sequencing, and molecular
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A,Residues: 1-315 «KRB»
A;Cross-references: EMBL:U24268; NID:g1171124; PIDN:AAC43575.1; PID:g1171125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPG-FEMITGPDLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQDRAFKNDKIDFIWSHTTKSINEKDGKVGS-----VTLTSTKDGSEETHEADGVFIYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.7%; Score 726; DB 1;
49.8%; Pred. No. 4.6e-47;
tive 50; Mismatches 96;
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**Kreimer, S.; Andreesen, U.R.

**Rubitted to the EMBL Data Library, April 1995

**A.Reference number: 863990
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Best Local Similarity 49.8
Matches 153; Conservative
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A; Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH C; Superfamily: thioredoxin reductase, thioredoxin reductase homology C; Superfamily: thioredoxin reductase; thioredoxin reductase; nomediant homodianer; NADP; oxidoreductase; redox-active disulfide F; 1-309/Domain: thioredoxin reductase homology cTRXBP.
F; 6-34/Region: beta-alpha-beta FAD nucleotide-binding fold F; 146-173/Region: beta-alpha-beta NADP nucleotide-binding fold F; 134-137/Disulfide bonds: redox-active #status predicted
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A,Residues: 1-307 <COL>
A,Cross-references: GB:AE001252; GB:AE000520; NID:g3323119; PIDN:AAC65780.1; PID:g332312
A,Experimental source: strain Nichols
                                                                                                                                                                                                                   Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjacession: C71279 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; (they, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 GYDPKSALVEGKLELDETGYIPTDDNWKTNVEGVFAAGDIRVKSLRQVVTATADGALAAV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTBEVENFPG-FEMITGPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable thioredoxin reductase (trxB) - syphilis spirochete
C,Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C,Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 LODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDG-----SEETHEADGVFIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Indels
A; Reference number: S63987; MUID:96096738; PMID:8529640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1;
1.5e-45;
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46.1%; Pred. No. 6.2e-45;
live 55; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Mismatches
                                                                                                            A;Cross-references: EMBL:U24268; NID:g1171124
C;Genetics:
A;Gene: trxB
A;Start codon: GTG
C;Complex: homodimer; each chain has a tightly
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.5%; Score 706;
48.5%; Pred. No. 1
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Matches 142; Conservative
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                                                      A; Molecule type: DNA
A; Residues: 1-117 < KRW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                  Accession: S63989
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Matches 150;
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A; Residues: 1-307
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thioredoxine reductase [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Date: B97007 Britoling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Fighly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Accession: B97007 A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA 
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C; Complex: homodimer; each chain has a tightly associated but noncovalently bound
C; Function:
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R,Mathieu, I.; Meyer, J.; Moulis, J.M.
R,Mathieu, I.; Meyer, J.; Moulis, J.M.
Bjochem. J. 285, 285-282, 1992
A;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sh;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sh;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sh;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sh;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sh;Title: Cloning, sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001437; PIDN:AAK78845.1; PID:g15023764; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.4%; Score 671;
ilarity 42.2%; Pred. No. 6:
Conservative 74; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAAEYIEH 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 130;
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A,Gene: CAC0869
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A;Accession: H72222
A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-317 <ARN>
A;Cxose-references: GB:AE001753; GB:AE000512; NID:g4981397; PIDN:AAD35951.1; PID:g49814G
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 PLIARPEKDLGITNDVGYIVTKDDMITSVPGIFRAGDVRDKGLRQIVTATGDGSLAAQSAA 302
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62
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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EIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEM-ITGP
                                                         C;Superfamily: thioredoxin reductase; thioredoxin reductase homology F;14-316/Domain: thioredoxin reductase homology <TRXB>
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Best Local Similarity 44.8%;
Matches 134; Conservative 6
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F;136-139/Disulfide bonds: redox-active #status predicted
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Length 308;	Indels	MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT	:   VGGQIRETYTV	61 GPDLSTKMFEHAKKFGA-VYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKI	:   :  EDVIYKVKALI	EEGTFTTKFAD	 EAAIFLTKYAR	LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYI	LQAQKYSQDELFKHKNVKIIMDSBIRNI-VGENEIEKIVVENVKTKQKTELKADGVFVYI	VRDKGLRQIVT	:  :   VRSKLIRQLIT		
	64; Mismatches 106; Indels	VLKTVMIERGI	<pre></pre>	EDKGEYKVINF	. :  :  CSDDEKILET	FVIGGGDSAV	VVVGGGNSAVEA	TEKDGKVGSVT		SVPGIFAAGD	:: :     FNIKGVFAAGD		
	64; Mismat	MTAAVYASRA	:	VYQYGDİKSVE	:  : : : :: IDQFSNIEKIF	CDGAFFKNKRI	:     ::   ELCDGALYQGKDI	FIWSHTTKSIN	  IWDSEIRNI-	THUCOXIVIYE	::    3YIETDENMET		
40.2%;	Conservative	TAIIGAGPAG	UIIGAGPAG	EHAKKFGA-	 EHAASIGVN	SGRGVSYCAV	: :    : IGKVIHYCEL(	RAFKNDKIDI	: ELFKHKNVK:	KDEGITNDV	  KDSININKW	5	ις
Query Match Best Local Similarity	134; Conse	. MGTEIDFD:	1 MKEEKQLDI	GPDLSTKME	GADLADKME	GVPGEQELC	PIPEEEKLE			GMKPLTAPE		300 SAAEYI 305	300 MAEKYI 305
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Search completed: September 15, 2004, 12:21:32 Job time: 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2004, 12:05:08 , Search time 23 Seconds (without alignments) 724.454 Million cell updates/sec Run on:

US-09-825-212-1 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	0000 [sylveto C[V900]	Scaping	DBORBO NECEDITATION /	1 icroria		Pibactor.	4,000	1 trenonema			092:02 ricketteia		_	DESCRIPTION OF COLUMN						arabidopsi	chiamydia	Opport chlamydia m		coxiella b		Co-110 Lasma		Vibrio cho	nelicopact	າ ເ	2002	4/348		P51978 neurospora
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	Score	1582				1054	726		697.5	•	4	641.5		632.5		5	619.5	605	601	598.5	595	593	81	564.5	64	564	558	558	554	552	51	50	545.5	44	:
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P75531 mycoplasma P38816 saccharomyc P57399 buchnera ap Q92375 schizosacch P43496 pentcillium P94284 borrelia bu Q89aj 2 buchnera ap P42974 bacillus su Q8264 pseudomonas Q8161 spironucleu Q99wj 7 staphylococ P26829 bacillus sp
TRXE MYCPN TRB2_YEAST TRXE BUCAI TRXE SCHPO TRXE BORBU TRXE BUCBP DHNA_BACSU AHPF PSEPK TRXE_STAAM DHNA_BACSP
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888888844444 45078860128845

## ALIGNMENTS

TERE STARM STANDARD, PRT; 311 AA.  TERE STARM (Rel. 43, Created) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence (Strain Nuls) 16-WAR-2004 (Rel. 43, Last sequence update) 16-WAR-2004 (Rel. 43, Last sequence update) 17 EAD STANN-MANSO (ARCC 700699, Red. 11804) 16 SEQUENCE FROM N.A. 16 SEQUENCE ROW N.A. 16 SEQUENCE ROW N.A. 16 SECHEMAN (M. Macupame A., Marakani H., Roboyashi I., Kanamani M., Matuyama A., Marukani M., Matuyama A., Marukani M., Matuyama A., Marukani M., Matuyama A., Marukani M., Matuyama A., Marukani M., Matuyama A., Marukani M., Matuyama A., Oshima K., Hirakawa H., Kubana M., Yamani M., Masun M., Yamani M., Masun M., Yamani M., Masun M., Yamani M., Yami M., Yami M., Yami M., Yami M., Yami M., Yami M., Yami M., Yami M., Yami M., Yami M.,
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Mol. Microbiol. 49:1577-1593(2003).
-;- CATALYTIC ACTIVITY: Thioredoxin
Microbiol. 49:1577-1593(2003).
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P80880. 006971;
01-NOV-1997 (Rel. 35, C.
15-MAR-2004 (Rel. 43, L.
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137
286
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302 DYITELKD 309
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NP BIND 35
DISULFID 134
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ses 278; Conserv
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SEQUENCE
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TRXB_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEGELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEBTHEADGVFIYIGMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228).";
                                           R PIR, E89649; E89849.

R HSSP, Q39243; 1VDC.

R HSSP, Q39243; 1VDC.

R SWISS-2DPAGE; Q99VL2; STAAN.

R INTEFPO; IPRO00759; Adradx reductase.

R INTEFPO; IPRO01327; FAD_DY_redox.

R INTEFPO; IPRO01037; FAD_DY_redox.

R INTEFPO; IPRO0103; PYLIdine_redox_2.

R INTEFPO; IPRO0103; PYLIdine_redox_2.

R INTEFPO; IPRO0109; PYL redox.

R PHAM: PRO0419; ADKNDTASE.

R PRINTS; PRO0469; PUNBUTASE.

R PRINTS; PRO0469; PUNBUTASEII.

R PRINTS; PRO0469; PUNBUTASEII.

R PRINTS; PRO0573; PYRALDINE REDOX_2; 1.

R PROSTITE; PS0573; PYRALDINE REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                   REDOX-ACTIVE (BY SIMILARITY) .
FAD (FLAVIN PART) (BY SIMILARITY)
1A337DE3736C9265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Score 1582; DB 1; Length 311; 99.4%; Pred. No. 3.1e-107; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                33616 MW;
              EMBL; AP003131; BAB41952.1; -. EMBL; AP004824; BAB94591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.4'
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYIEHLNDQA 312
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137
286
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311 AA;
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STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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Q8CPY8;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DLSTRWFEHARKFGAEYQYGDIKSVEDKGDYRVINLGNKEITAHAVIISTGAEYRKIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEQELGGRGVSYCAVCDGAFFKNKRLFV1GGGDSAVEEGTFTTKFADKVT1VHRRDELRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                     -1. COPACTOR: Binds 1 FAD per subunit (By similarity).
-1. SUBUNIT: Homodimer (By similarity).
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. MISCELLANBOUS: The active site is a redox-active disulfide bor -1. SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AEO16745; AAO04144.1; -.

R InterPro; IPR000759; Adrndx_reductase.

R InterPro; IPR0001327; FAD_pyr_redox.

InterPro; IPR001327; FAD_pyr_redox.

InterPro; IPR008255; Pyr_redox_2.

R InterPro; IPR008255; Pyr_redox_2.

R InterPro; IPR008255; Pyr_redox_reduct.

R Pfm1; PR0070; Pyr_redox_reduct.

R PRINTS; PR00369; PADPRN.

R PRINTS; PR00369; PADPRN.

R PRINTS; PR00469; PNDROTASEII.

R TIGRAMS; IGR01292; TRX_reduct; 1.

R PROSITE; PS00573; PYRIDINE_REDOX_2; 1.

R Redox_active_center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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REDOX-ACTIVE (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY)
DSD6853667137D8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5%; Score 1455; DB 1; Length 310; 90.3%; Pred. No. 4.6e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
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Last sequence update)
Last annotation update)
           + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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RA Kunst F., Ogasawara N. Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.
RA Deceded V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Göffeau A., Galistin R., Hander D., Tarani G., Harwood C.R., Henaut A.,
RA Ghim S.Y. Kanamata D., Kasahara Y., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Mones L.,
RA Koris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardhoots S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Kumano M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Scholin A., Tacconi E., Roche E., Roche M., Schole B.,
RA Scholin J., Sekowska A., Seror S.J., Serror P., Schole B.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier R., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Tognoni A.,
Vari A., Wambutt R., Wedler E., Wedler H., Weitzeneger T., R.
Whiters P., Mipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Rattines P., Mipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Rattines P., Whiters P., Wedler E., Wedler H., Weitzeneger T.,
Rattines P., Willers P., Wedler E., Wedler H., Weitzeneger T.,
Rattines P., Willers P., Wedler E., Wedler H., Weitzeneger T.,
Rattines P., Willers P., Wedler E., Wedler H., Weitzeneger T.,
Rattines P., Willers P., Wedler E., Wedler H., Weitzeneger T.,
Rattines P., Weitzeneger T., Takerin Bacillus
Rattines P., Weitzeneger T., Yamanoto H., Yamane K., Yasumoto P., Wehler B., Weitzeneger T.,
Rattines P., Weitz
      (EC 1.8.1.9) (TRXR) (General stress protein 35)
                                                                                                                                                                                                   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                      Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
      Thioredoxin reductase
                                                                                  Bacteria; Firmicutes;
NCBI_TaxID=1423;
                                                             Bacillus subtilis.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                              OR BSU34790
                                                                                                                                                                  STRAIN=168;
                                                                                                                                                                                                                                                                       STRAIN=168;
                                                                                                                                                                                       Denizot F.
                                              TRXB
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"First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997)
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                       STRAIN=168 / ISS8,
MEDLINE=97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
SEQUENCE OF 1-23
                                                                                                                                  Hecker M.;
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-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-:- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
limitation and oxygen limitation
-:- MISCELLANEOUS: The active site is a redox-active disulfide bond (By similarity) -!- COFACTOR: Binds 1 FAD per subunit (By similarity). oxidoreductase family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 PFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                               134 137 REDOX-ACTIVE (BY SIMILARITY).
277 286 FAD (FLAVIN PART) (BY SIMILARITY).
1 5 - A (IN REF. 3).
5 6 7 -> E (IN REF. 3).
315 AA; 34388 MW; 1BED957C979AE2AC CRC64;
                                                                                                                                                                               PRINTS, PRO0368; FADENR.
PRINTS, PRO0411; PNDEDTASEI.
PRINTS, PRO0469; PNDEDTASEI.
TIGREPAMS, TIGRO1292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                     FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                             Length 315;
                                                                                                                                                                                                                                                                                                                                                                 69.4%; Score 1154; DB 1; Length 3
71.4%; Pred. No. 2.5e-76;
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NCBI TaxID=1642;
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                                                       HSSP, 039243; 10DC.
Subtilist, BG12399; trxB.
InterPro; IPR001759; Adradx reductase.
InterPro; IPR001327; FAD_pyr redox.
InterPro; IPR001327; FAD_pyr redox.
InterPro; IPR001825; Pyr redox.
InterPro; IPR001825; Pyr redox.
InterPro; IPR005982; Thioredox_reduct.
Pfam; PF00070; pyr redox; I.
PRNNTS; PR00419; ADXRDTASE.
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  email to license@isb-sib.ch)
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28-FEB-2003 (Rel. 41, Created)
                     EMBL; Z99121; CAB15484.1; -.
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Best Local Similarity 71.4%
Matches 220; Conservative
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                                                PIR; A69727; A69727
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SEQUENCE FROM N.A.
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DISULFID
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CONFLICT
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HSSP; 039249)
Listilist; LM002478; -.rdx reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF009622; AAB63804.1; -. EMBL; AL591983; CAD00556.1; -.
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                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                         HLND 310
                                                                                                                                              308 ELKE 311
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CTRAIN=CLIP 11262 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Baqueror F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Cherbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Bomann E., Dominguez-Bernal G., Duchaud E., Durant L., Deboux P.,

Brian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

A Gutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerset U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsieß G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Nazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMFEHAKKEGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
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-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                               -:- COFACTOR: Binds 1 FAD per subunit (By similarity).
-:- SUBCHLIGAR LOCATION: Cytoplasmic (By similarity).
-:- SUBCELLANGAR LOCATION: Cytoplasmic (By similarity).
-:- MISCELLANBOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
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PRINTS; PRO0469; PURBUTASEII.
TIGGRAMS; TIGGRO1292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD (ADP PART) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listilist, LIN02621; -
LinterPro; IPR000799; Adrndx_reductase.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR00103; Pyr_redox_AS.
InterPro; IPR00103; Pyridine_redox_LinterPro; IPR005982; Thioredox_reduct.
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PIR; AH1759; AH1759.
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
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SEQUENCE
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MEDINE_ZOUST, DebMed=11679669;

MEDINE_ZOUST, PubMed=11679669;

MEDINE_ZOUST, PubMed=11679669;

MEDINE_ZOUST, BuchTieser C., Rusniok C., Amend A.,

MEDINE_ZOUST, BuchTieser C., Rusniok C., Amend A.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

MEDINE_ZOUST, MEDINEL Garcia-del Portillo F., Garrido P.,

MEDINE_C. M., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Andueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Narquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

"Comparative Genomics of Listeria species.";

"CATALITIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
188 QDRAFKDEKUDFIMNNTVEELIGDGKKVTSVKLVSTVDGSESIMPVDGVFIXVGLVPLTK 247
                                                                                                                                        248 AFLSLGITDEEGYIVTDEEMRTNLPGIFAAGDVRAKSLRQIVTATGDGGLAGONAQKYVE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrovok I., Mislovati M., Cohen G., Aharonowitz Y.; "Isolation, cloning and characterization of the Listeria monocytogenes
                                                                                              247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBBUILT: Homodimer (By similarity).
-:- SUBCELLANEOUS: Cytoplasmic (By similarity).
-:- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thioredoxin reductase gene, trxB.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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                                                                                                                                                                                                                                                                          126
                                                                                                                                                                                                                                                                               LGGRGYSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
                                                                                                                                                                                                                                                                                                                    QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                                                                                                                                247 PFKDLGIINDVGYIVIKDDMITSVPGIFAAGDVRDKGLRQIVTAIGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                                     248 AFLNLGITDDEGYIVTDEEMRINLPGIFAAGDVRAKSLRQIVIATGDGGLAGQNAQKYVE 307
                                                                                                                                                                                                                                            YDVIIIGAGPAGMTAALYISRADLDTLMIERGVPGGGWVNTAEVENYPGFDSILGPDLSD 67
                                                                                                                                                                                                                          7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPPGFEMITGPDLST
                                                                                                                                                                                                                                                                 67 KMFEHAKKEGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luebbers M., Andreesen J.R.; "Components of glycine reductase from Eubacterium acidaminophilum. Cloning, sequencing and identification of the genes for thioredoxin reductase, thioredoxin and selenoprotein PA."; Elochem. 217:791-798(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eubacterium acidaminophilum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
                                                                                                                                                                                                             0
                                                                                                                                   FAD (ADP PART) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY); 8D42F36970611979 CRC64;
                                                                                          TIGRFAMS; TIGRO1292; TRX reduct; 1.
PROSITE; PS00573; PYRLDINE REDOX 2; 1.
Redox-active center; Oxidoreductāse; NADP; Flavoprotein; FAD;
Complete proteome.
                                                                                                                                                                                     Query Match 63.4%; Score 1054; DB 1; Length 319; Best Local Similarity 65.5%; Pred. No. 4.3e-69; Matches 199; Conservative 43; Mismatches 62; Indels
                                                                                                                                                                                                             62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISION TO 275.
Andreesen J.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                ; Pred. No. 4.3e-69; 43; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 AA
InterPro; IPR000103; Pyridine_redox_2.
InterPro; IPR003042; Rng_mnoxygenase.
InterPro; IPR005982; Phioredox_reduct.
Pfam; PF00070; pyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00419; PADPR.
PRINTS; PR00461; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=DSMZ 3953;
MEDLINE=94039119; PubMed=8223622;
                                                                                                                                   44 FAL
139 REI
288 FAL
; 34173 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                 319 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  HLND 310
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136
279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eubacterium.
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P50971;
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                                                                                                                                                                SEQUENCE
                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 LODRAFKNDKIDFIWSHTTKSINEKDGKVGS-----VTLTSTKDGSEETHEADGVFIYI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                       Freundenberg W., Dietrichs D., Lebertz H., Andreesen J.R., "Isolation of an atypically small lipoamide dehydrogenase involved in the glycine decarboxylase complex from Bubacterium acidaminophilum.", J. Bacteriol. 171:1346-1354(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPG-FEMITGPDLS
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                                                                                                                                                                                                                                                                                                                                                                     -: SUBCULIT: Homodimer (By similarity).
-: SUBCELLUIGAR LOCATION: Cytoplasmic (By similarity).
-: SUBCELLUIGAR LOCATION: Cytoplasmic (By similarity).
-: MISCELLANBOUS: The active site is a redox-active disulfide bond.
-: SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
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R InterPro; IPR001327; FAD_DYT_redox.

InterPro; IPR001327; FAD_DYT_redox.

R InterPro; IPR00103; Pyridine redox2.AS.

R InterPro; IPR00103; Pyridine redox2.

R InterPro; IPR00103; Pyridine redox2.

R InterPro; IPR00104; Pyridine redox2.

R PRINTS; PR00419; ADXRDTASE.

R PRINTS; PR00419; ADXRDTASE.

R PRINTS; PR00419; PADPRASE.

R PRINTS; PR00419; PADRATASEI.

R PRINTS; PR00416; PADRATASEI.

R PRINTS; PR00469; PADRATASEI.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

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R PRINTS; PR00469; PADRATASEII.

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R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

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R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

R PRINTS; PR00469; PADRATASEII.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.7%; Score 726; DB 1; Length 31
49.8%; Pred. No. 2e-45;
iive 50; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145B0EABB2B8A7FA CRC64;
MEDLINE=89155433; PubMed=2537814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 291 F
315 AA; 34033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L04500; AAB93303.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 QAEKYVE 310
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                                                                                                                                                                                                                                                                                            NADPH.
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Pfam; PF00070; pyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                                                                                                                     TRXB OR TP0814
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                              -:- COFACTOR: Binds 1 FAD per subunit (By similarity).
-:- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Gytoplasmic (By similarity).
-!- MISCELLANBOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; 039243; 19020.

R InterPro; IPR000759; Adrndx_reductase.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001013; PyrIdine_redox_2.

R InterPro; IPR001013; PyrIdine_redox_2.

R InterPro; IPR001013; PyrIdine_redox_1.

R InterPro; IPR001013; PyrIdine_redox_1.

R InterPro; IPR001013; PyrIdine_redox_1.

R Rinrs; PR00419; ADXRDTASE.

R RINRS; PR00419; ADXRDTASE.

R RINRS; PR00419; PNDRDTASEI.

R RINRS; PR00419; PNDRDTASEI.

R RINRS; PR00411; PNDRDTASEI.

R RINRS; PR00411; PNDRDTASEI.

R REDOx_2: 1.

R REDOx_2: 1.

R REDOx_ACTIVE (BY SIMILARITY).

R BIND

R 137 REDOX_ACTIVE (BY SIMILARITY).

R SEQUENCE 315 AA; 33946 MM; 2CA55D36E579E2EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
8
                                                                                                  Clostridium litorale (Bacterium W6).
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.5%; Score 706; DB 1;
48.5%; Pred. No. 5.6e-44;
                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
TRXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.5%; Pred. nv.
                       Ā
                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=96096738; PubMed=8529640;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U24268; AAC43575.1; -. PIR; S63990; S63990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 150; Conservative
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                          NCBI_TaxID=1557;
                                                                                                                                Clostridium
                                                                                                                                                                                                                                                             + NADPH
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                                                                                                                                                                                                                                                                              240 GMKPLTAPPKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                               244 GYDPKSALVEGKLELDETGYIPTDDNMKTNVEGVFAAGDIRVKSLRQVYTATADGAIAAV 303
ELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRDELRAQRI 185
                                               MEDLINE=9833770; PubMed=965876; MEDLINE=9833770; PubMed=965876; Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Praser C.M., Norris S.J., Weinstock G.M., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                       LQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDG-----SEETHEADGVFIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treponema pallidum.
Bacteria: Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- MISCELLANEOUS: The active site is a redox-active disulfide bot
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR00103; Pyr_redox2.
InterPro; IPR00103; PyrIdine_redox2.
InterPro; IPR005982; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001252; AAC65780.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        300 SAAEYIEHL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 QAEKYIEEL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C71278; C71278
HSSP; Q39243; 1VDC.
TIGR; TP0814; -.
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                                                                                                                                                                                                                                                                                                                                                                                              63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLTAPFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PITGLLPD-AEKDSTGYIVTDDEMRTSVEGIFAAGDVRAKSFRQVITATSDGALAAHAAA 299
                                                                                                                                                                                                                                                                                                                4 EIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEM-ITGP 62
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing and expression in bolders.";
rubredoxin gene from Clostridium pasteurianum.";
Blochem. J. 285:255-262(1992).
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                    3
      PRINTS; PRO0469; PNDEDTASEII.

TIGRFAMS; TIGR01292; TRX_reduct; 1.

PROSITE; PS00573; PYRIDINE_REDOX_2; 1.

Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; Flavoprotein; FAD; NADP; FAD; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FADP; FAD
                                                                                                                                  FAD (ADP PART) (BY SIMILARITY).
PADOX-ACTIVE (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY).
2519A5BA3BB4E012 (RC64;
                                                                                                                                                                                                                                        DB 1; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 2.2e-43;
55; Mismatches 108; Indels
                                                                                                                                FAD (ADP PART) (BY
                                                                                                                                                                                                                                  42.0%; Score 697.5;
46.1%; Pred. No. 2.2e
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                                                                                                                                                                                          32868 MW;
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01-NOV-1991 (Rel. 20, Last seq
  PR00411; PNDRDTASEI. PR00469; PNDRDTASEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60116; AAA23276.1; -. PIR; S29117; S29117.
HSSP; Q39243; 1VDC.
                                                                                                                                                                                                                                                                       Matches 142; Conservative
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137
284
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                                                                                                                                                                                    307 AA;
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                             134
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NCBI_TaxID=1501;
                                                                                                                                             DISULFID
NP_BIND
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                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                             Query Match
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                                                                                                                              BIND
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P23160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 PIPEBEKLHGKVIHYCELCDGALYQGKDLVVVGGGNSAVEAAIFLTKYARNITIVHQFDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIXI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 GMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                         Flavoprotein; FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
R InterPro; IPR000759; Adrndx reductase.
R InterPro; IPR001327; FAD_pyr_redox.
R InterPro; IPR001100; Pyr_redox.
R InterPro; IPR00100; Pyr_redox.
R InterPro; IPR000103; Pyr_idine_redox_2.
R InterPro; IPR000103; Pyr_idine_redox_2.
R PRINTS; PR00419; ADXRDTASE.
R PRINTS; PR00419; ADXRDTASE.
R PRINTS; PR00469; PNDRDTASEI.
R PRINTS; PR00469; PNDRDTASEI.
R PRINTS; PR00469; PNDRDTASEI.
R PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DISCUED.
N Redox-active center; Oxidoreductase; NADP; NAD; Flavoprotein DISCUED.
IN PRINT 26 279
REDOX_ACTIVE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Thioredoxin-thioredoxin reductase system of Streptomyces clavuligerus: sequences, expression, and organization of the J. Bacteriol. 175:5159-5167(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae; Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abaronowitz Y., Av-Gay Y., Schreiber R., Cohen G.;
"Characterization of a broad-range disulfide reductase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 43.8%; Pred. No. 3e-41;
Matches 134; Conservative 64; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-32.
STRAIN=ATCC 27064 / DSM 738 / NRRL 3585,
MEDLINE=93352422; PubMed=8349555;
Cohen G., Yanko M., Mislovati M., Argaman A., Schreiber Av-Gay Y., Aharonowitz Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 AA; 34215 MW; 52D9CF51208EFC37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD (FLAVIN PART)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07N-1994 (Rel. 29, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.2%; Score 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE=93139027; Pubmed=8423136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Q05741;
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TRXB STRCL
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                                                                                                                      TRXB OR RC0618.
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                                               RICCN
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                                                           Q92I02;
                        RESULT 11
TRXB_RICCN
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TKMPEHAKKFGAVYQYGDIKSVEDKGEYK-VINFGNKELTAKAVIIATGAEYKKIGVPGE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 QELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 ILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPFKDLGITNDVGYI-VTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 TELFKGQLDLDDEGYLKVASPSTRTNLTGVFAAGDVVDHTYRQAITAAGTGCSAALDAER 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 DIALIGAGPAGMTAAVYASRANLKTVMIERGI-PGGQMANTEEVENFPGF-EMITGPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                               disulfide redox balance.
CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                               -:- SUBUNIT: Homodimer.
-:- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
           stribiotic biosynthesis.";
J. Bacteriol. 175:623-629(1993).
-!- FUNCTION: Component of the thioredoxin-thioredoxin reductase system which may be involved in biosynthesis of penicillins are cephalosporins and may be important in determining the thiol-
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ري
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY)
4C2B01AADC5A0FDF CRC64;
Streptomyces clavuligerus and its possible role in beta-lactam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%; Score 644.5; DB 1; Length 321; 45.6%; Pred. No. 1.6e-39; tive 53; Mismatches 109; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAD (ADP PART) (BY SIMILARITY).
                                                                                                                -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                           InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001327; PAD_pyr_redox.
InterPro; IPR001805; Pyr_redox.
InterPro; IPR008255; Pyr_redox2.
InterPro; IPR000139; PyrIdine_redox_2.
InterPro; IPR005982; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AA; 34015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
                                                                                                                                                                                                                                                                                          EMBL; Z21946; CAA79940.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00070; pyr redox, 1
PRINTS; PR00419; ADXRDTASE.
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                                                                                                                                                                                                                                                                                                       PIR; A53307; A53307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                    HSSP; P09625; 1CLO.
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
-!- CATALYIIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNTT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLARBOUG: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
MGDLINE=21442074; PubMed=11557893;
MGDLINE=21442074; PubMed=11557893;
MGDGata H., Audic S., Renestc-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAD (ADP PART) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
                                                                                                                                                                                                                        Rickettsia conorii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%; Score 641.5; DB 1;
46.0%; Pred. No. 2.5e-39;
tive 45; Mismatches 107;
                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001355; Pyr_redox.2.
InterPro; IPR001359; Pyr_redox.2.
InterPro; IPR005981; Thioredox_reduct.
Pfam; PF00070; pyr_redox; I.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00461; PADRUTASEI.
PRINTS; PR00461; PNDRUTASEII.
                                                                                                                                                                                                                                                                                    Rickettsiaceae, Rickettsieae, Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008622; AAL03156.1; -. PIR; B97777; B97777.
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Matches 144; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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3D0DD581E6C187E2 CRC64;
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V -> C (IN REF. 1).
V -> Y (IN REF. 1).
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46.4%; Pred. No. 3.9e-39;
                                                                                                                                                                                                                                                                                                                                         Tuberculist, Rv3913; -
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001327; FAD_Dyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR01100; Pyr_redox.
InterPro; IPR001100; Pyr_redox2 As.
InterPro; IPR000103; PyrIndine_redox 2.
InterPro; IPR000103; PyrIdine_redox 2.
InterPro; IPR005982; Thioredox_reduct.
PRINTS; PR00019; ADXRDTASE.
PRINTS; PR0019; ADXRDTASE.
                                                                                                                                                                                                                                        EMBL, AL021426; CAA16226.1; --
Embl. ARE007194; ARK48397.1; --
PIR; A70851; A70851
HSSP, Q39243; 1VDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
                   oxidoreductase family.
                                                                                                                                                                                                                       EMBL; X95798; CAA65070.1;
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148
297
125
215
228
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215
228
335 AA;
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                                                                                                                                                                                                                                                                                                                          TIGR; MT4032;
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                                        PGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELR 181
                                                                                                                                                          AEKILQDRLFRNSKISVIWDHVVDEI-----VGSNKPKSVTGVKIQNVHTKEISLLNCS 235
                                                                                                                                                                                                  GVFIYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-ŢSVPGIFAAGDVRDKGLRQIVTATG 292
                                                                                                                                                                                                                                62 WLMEQMYMQAKNVGTEIVSDYVEKVDLSKRPFKVFTGAGNEYDAESIIICTGAEAKWLGI 121
                                                             182 AQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGS---VTLTSTKDGSEETHE----AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s:
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-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis and funtional characterization of thioredoxin and thioredoxin reductase of Mycobacterium tuberculosis.", Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22206494; PubMed=12218036; Retain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To Strain To S
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-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-8829597; PubMed-9534230; Cole S.T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gardon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Hornsby T., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Seeger K., Skelton S., Squares M., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wieles B., Phillip W., Drijfhout J.W., Offringa R., Ottenhoff T.H.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                    DGSIAAQSAAEYI 305
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SEQUENCE FROM N.A.
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PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Mismatches 104; Indels
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ID TRXB MYCLE
AC P46843;
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InterPro; IPR005746; Thioredoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Bifunctional thioredoxin reductase/thioredoxin [Includes: Thioredoxin reductase (EC 1.8.1.9) (TRXR); Thioredoxin].
TRXB/A OR TRX OR ML2703.
                                                                                                                                                                                                                                                                                                      MEDLINE=97124199; PubMed=8969512; Feihi H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takiff H.B., Eiglmeier K., Bergh S., Cole S.T.; Generangement and organization in an approximately 76 kb fragment encompassing the oriC region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Unique gene organization of thioredoxin and thioredoxin reductase in Mycobacterium leprae.";
Mol. Microbiol. 16:921-929(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bound.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide.
                                                                                                                                                                                  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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InterPro; 1PR001327; FAD pyr redox.
InterPro; 1PR001100; Pyr_redox.
InterPro; 1PR001015; Pyr_redox.
InterPro; 1PR000103; PyrIdine_redox_2.
InterPro; 1PR000663; PyrIdine_redox_2.
InterPro; 1PR006663; Thioredox dom2.
InterPro; 1PR00663; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=96059638; PubMed=7476189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:3147-3161(1996)
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HSSP; P80579; 1QUW.
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EMBL; X87899; CAA61150.1; -.
                                                                                                                                                                     Mycobacterium leprae
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MEDLINE=99014240; PubMed=9795152;

Gal-Mor O., Borovok I., Av-Gay Y., Cohen G., Aharonowitz Y.;

Gene roganization in the trxA/B-oriC region of the Streptomyces

coelicolor chromosome and comparison with other eubacteria.";

Gene 217:83-90(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                 THIOREDOXIN.

FAD (ADP PART) (BY SIMILARITY).

REDOX.ACTIVE (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY)

REDOX.ACTIVE (BY SIMILARITY).

84D367AB31899987 CRC64;
                          PRINTS; PRO04619; ADXRDTASE.
PRINTS; PRO0419; ADXRDTASE.
PRINTS; PRO0411; PNDRDTASEI.
PRINTS; PRO04211; PHORDTASEI.
PRINTS; PRO0421; THOREDOXIN.
TIGRFAMB; TIGR01068; thioredoxin; 1.
TIGRFAMB; TIGR01292; TRX reduct; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
PROSITE; PS00573; PXRIDINE_REDOX_2; 1.
PROSITE; PS00573; PXRIDINE_REDOX_2; 1.
Redox_active_center; Oxidoreductase; NADP; Flavoprotein; FAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Score 632.5; DB 1; Length 458; 45.3%; Pred. No. 1.8e-38;
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                                                                                                                                                                                                                                                                     THIOREDOXIN REDUCTASE
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30-MAY-2000 (Rel. 39, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                               LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                               49046 MM;
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Pfam; PF00070; pyr_redox; 1.
Pfam; PF00085; thiored; 1.
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294
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142
285
379
458 AA;
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Best Local Similarity
Matches 140; Conserv
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Matches 136; Conservative
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                                                           Similarity
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FAD (ADP PART) (BY SIMILARITY).

FREDOX-ACTIVE (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

A -> R (IN REF. 1; CAA63075/CAA07451).

ER -> DG (IN REF. 1; CAA63075/CAA07451).

MISSING (IN REF. 1; CAA63075).

MISSING (IN REF. 1; CAA63075).

WISSING (IN REF. 1; CAA63075).

F -> R (IN REF. 3).

P -> R (IN REF. 3).
                                                                                                                                                                          STRAIN=A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Marchar S. Chatler K.F., Cardeno-Tarraga A.-M., Kieser H., Harris D.E., Quail M.A., Kieser H., Kieser T., Larke L., Murphy L., Oliver K., Owall S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Reger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xre 41/:141-14/(2002).
CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLAREOUS: The active site is a redox-active disulfide bond.
SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).", Nature 417:141-147(2002).
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PROSITE; PS00573; PVRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                      Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
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EMBL; X92104; CAA63075.1;

EMBL; AL07313; CAA6431.1;

EMBL; AL93118; CAA63741.1;

PIR; T3657; T3657;

PIR; T42062; T42062.

HSSP; Q39243; 1VDC.

INTERPO; IPRO01759; Adrndx reductase.

INTERPO; IPRO0137; FAD pyr redox.

INTERPO; IPRO0137; FAD pyr redox.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

INTERPO; IPRO0100; Pyr redox2.

Pfam; PF00070; Pyr redox1.

PRINTS; PRO0410; Pyr redox2.
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34024 MW;
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PRINTS; PR00469; PNDRDTASEII
TIGRFAMS; TIGR01292; TRX_redi
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138
287
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                                                        STRAIN=A3(2) / M145;
                                                                                                                                                            SEQUENCE FROM N.A
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REVISIONS.
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                                                                                                                                                                                                                                                                                                            185 ILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEFTHEADGVFIYIGMKPL 244
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                                                                                                                                                                                                                                                        TAPFKDLGITNDVGYI-VTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAE 303
                                                                                                                                                                                                                                                                                                                                                                                                                244 TELFKGQLDLDPBGYLKVDAPSTRINLTGVFGAGDVVDHTYRQAITAAGTGCSAAVDAEP 303
                                                                                       65
                                                                                                                            64
                                                                         8 DIALIGAGPAGMTAAVYASRANLKTVMIERGI-PGGQMANTEEVENFPGF-EMITGPDLS
                                                                                                             5 NVIIIGSGPAGYTAALYTARASLKPLVFEGAVTAGGALMNTTEVENFPGFQDGIMGPELM
                                                                                                                                                                            | |::||| | :::||| DDDVVAVDLSGEIKTVTDTAGTVHRAKAVIVTTGSQHRKLGLPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 396:133-140(1998).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNT: Homodimer [By similarity].
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- MISCELLANEOUS: The active site is a redox-active disulfide bon
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                5
          Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
37.6%; Score 625.5; DB 1;
43.7%; Pred. No. 3.8e-38;
live 56; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-WAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
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us-09-825-212-1.rsp

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182 AQRILQDRAFKNDKIDFINSHTTKSINEKDGKVGSVTLTSTKDGSEETHE-----ADGVF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AEKILQDRLFKNPKISVIWDHI----IDEIVGSNKPRAVTGVKIQNVYTNEINLVNCSGVF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 IYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 IAIGHAPNTALFKGQIAIDDDNYIVTQSGSTRTNVBGVFAAGDVQDKIYRQAVTAAASGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 PGEGELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 DLSTKMFEHAKKFGAVYQYGDIKSVE-DKGEYKVINFGNKELTAKAVIIATGAEYKKIGV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                    37.3%; Score 619.5; DB 1; Length 310;
45.2%; Pred. No. 9.8e-38;
ative 48; Mismatches 111; Indels 11; Gaps
InterPro; IPR001327; FAD_pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001003; Pyr_redox2 AS.

InterPro; IPR0010103; Pyr_redox2.

InterPro; IPR0010103; Pyr_redox2.

InterPro; IPR0010103; Pyr_redox_reduct.

R Ffam; PP00070; pyr_redox; 1.

R PRINTS; PR00411; PNDRDTASE.

R PRINTS; PR00411; PNDRDTASE.

R PRINTS; PR00411; PNDRDTASEI.

R PRINTS; PR00411; PNDRDTASEI.

R PRINTS; PR00411; PNDRDTASEI.

R PROSTEE; PS00573; PYRIDINE REDOX 2; 1.

W Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;

M Complete proteome.
                                                                                                                                                                                                                                                     PAD (ADP PART) (BY SIMILARITY).
REDOX.ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY);
573CA975C750957D CRC64;
                                                                                                                                                                                                                                                            34 41 FAI
135 138 REI
281 290 FAI
310 AA; 33582 MW; 5
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Best Local Similarity 45.2%
Matches 140; Conservative
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299 MAALEVAKFL 308
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SEQUENCE
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Search completed: September 15, 2004, 12:16:34 Job time : 24 secs

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September 15, 2004, 12:12:53; Search time 115 Seconds (without alignments) 877.964 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                      1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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sp_bacteria:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mcsmc1:*
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sp_phage:*
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sp_bacteriap:*
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sp_rodent:*
sp_virus:*
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Perfect score:
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## ALIGNMENTS

XC STRAIN=RUSA277;
XX MEDINE=20031141; PubMed=10566865;
Ad elencastre H., Wu S.W., Plinho M.G., Ludovice A.M., Filipe S.,
Ad elencastre H., Wu S.W., Plinho M.G., Ludovice A.M., Filipe S.,
Ad dardete S., Sobral R., Gill S., Chung M., Tomasz A.;
Antibiotic resistance as a stress response: complete sequencing of a large number of formomognal loci in Staphylococous aureus strain COL RI Intel impact on the expression of resistance to methicillin.";
Additional Resist. 5:163-175(1999).
REMBL, ALS27881; CAB60740.1;
BR EMBL, ALS3781; CAB60740.1;
BR FIRE, E89849; E89849.
BR HSSP; O39243; 1VDC.
BR GG: GG:0005737; C:cytoplasm; IEA. Uziel O., Borovok I., Schreiber R., Aharonowitz Y., Cohen G.,
"Transcriptional analysis of the thioredoxin (trxA) and thioredoxin
reductase (trxB) genes from Staphylococcus aureus.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. 01-JUN-1998 (TrEMBLrel. 06, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Thioredoxin reductase (EC 1.6.4.5) (Thioredoxine reductase). Borovok I.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. Staphylococcus aureus. Bacteria; Firmicutes; Bacillales; Staphylococcus. NCBI\_TaxID=1280; 311 AA. PRT; PRELIMINARY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=Oxford; O54079; Q9RL89 STRAIN=Oxford; 054079 RESULT 1 054079 DDR ND DE NOTE OF STREET O

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Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; PADPNE.
PRINTS; PR004411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
TIGRFAMS; TIGR01292; TRX reduct; 1.
PR0SITE; PS00673; PYRIDINE REDOX 2; 1.
PR05; Flavoprotein; Oxidoreductase; Complete protecome.
SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;
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                                                 Lancet 357:1225-1240(2001)
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Best Local Similarity 99.4
Matches 308; Conservative
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           R GO; GO: 0015036; F: disulfide oxidoreductase activity; IEA.

R GO; GO: 0004791; F: thioredoxin-disulfide reductase activity; IEA.

R GO; GO: 0004791; F: thioredoxin-disulfide reductase activity; IEA.

GO; GO: 0019430; P: removal of taperoxide radicals; IEA.

R InterPro; IPR001327; FAD pyr redox.

R InterPro; IPR00137; FAD pyr redox.

InterPro; IPR001031; PyrIdia_redox_2.

InterPro; IPR008255; Pyr redox.

InterPro; IPR008255; Pyr redox.

InterPro; IPR008255; Pyr redox.

INTERPRO; IPR0083821; Thioredox_reduct.

PRINTS; PR00419; ADXRDTASE.

PRINTS; PR00419; PNDRDTASEI.

PRINTS; PR00419; PNDRDTASEI.

IGRFAMS; TIGR01292; TRX_reduct; 1.

PROSITE; PR00533; PYRIDINE_REDOX_2; 1.
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                                                                                                                                                                                                                                                                    311 AA; 33616 MW; 1A337DE3736C9265 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxine reductase.
Thioredoxine xequences.
Staphylococcus aureus (strain NW30 / ATCC 700699),
Staphylococcus aureus (strain NW315), and
Staphylococcus aureus (strain NW315).
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NCBI_TaxID=158878, 158879, 196620;
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Lancet 359:1819-1827(2002).

--- COFACTOR: FAD (BY SIMILARITY).

--- COFACTOR: FAD (BY SIMILARITY).

EMBL; AP003306; BAB5626.1; ---

REMBL; AP003131; BAB44591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BAB94591.1; ---

REMBL; AP004824; BR98041; Fithioredoxin-disulfide reductase activity; IEA.

RO; GO:0004191; P:thioredoxin-disulfide radicals; IEA.

RITERPRO; IPR001327; FAD pyr_redox.

RITERPRO; IPR001327; FAD pyr_redox.

RITERPRO; IPR00100; Pyr_redox.

RITERPRO; IPR008255; Pyr_redox.

RITERPRO; IPR08255; Pyr_redox.

RITERPRO; IPR08255; Pyr_redox.

RITERPRO; IRR08255; Pyr_redox.

RITERPRO; IRR08255; Pyr_redox.

RITERPRO; IRR08255; Pyr_redox.

RITERPRO; IRR08255; Pyr_redox.

RITERPRO; IPR08255; Pyr_redox.

RITERPRO; IPR08255; Pyr_redox.

RITERPRO; IPR08255; Pyr_redox.
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
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R GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

R GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

R GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.

GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:removal of superoxide radicals; IEA.

InterPro; IPR001137; FAD_pyr_redox.

R InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001555; Pyr_redox.

InterPro; IPR001592; Thioredox_reduct.

R Pfam; PF00070; pyr_redox; 1.

R PRINTS; PR00368; FADPNR.
                                                                                                                                        MEDLINE=20031141; PubMed=10566865,

de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S.,

de Zendete S., Sobral R., Gill S., Chung M., Tomasz A.;

"Antibiotic resistance as a stress response: complete sequencing of large number of chromosomal loci in Staphylococcus aureus strain (
that impact on the expression of resistance to methicillin.";

Microb. Drug Resist. 5:163-175(1999).

EMBL; Y14324; CAB82468.1; -

HSSP; Q39243; 1VDC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1487; DB 2; Length 291;
Pred. No. 1e-97;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIEHLNDQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 AA; 31640 MW; 3C700EE8752343CF CRC64;
          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                               Hypothetical protein (Fragment).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%;
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00411; PNDRDTASEL PRINTS; PR00469; PNDRDTASEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.3
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Thioredoxine reductase.
                                                                                                                 SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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ID Q8CPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEBGTFLTKFADKVTIVHRRDELRA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK
                                                                                                                                                                                                                                                                                 L., Lu G., Jia J., Tu Y., Qin Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                         EMBL, ARO16735; AA004144.1; Coytoplasm, IEA.
GO, GO:0005737; C:cytoplasm, IEA.
GO, GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO, GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO, GO:0006118; P:electron transport; IEA.
GO, GO:0019430; P:removal of superoxide radicals; IEA.
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                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thioredoxin reductase.
TRXB OR BAS387.
Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 AA; 33544 MW; D5D6853667137D8B CRC64;
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25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 87.5%; Score 1455; DB 16; Local Similarity 90.3%; Pred. No. 2.1e-95; les 278; Conservative 17; Mismatches 13;
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAM; PF00070; Dyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
TIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000759; Adrindx reductase.
InterPro; IPR001327; PAD pyr redox.
InterPro; IPR000103; Pyridine_redox_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001100; Pyr redox.
InterPro; IPR008255; Pyr redox2 AS.
InterPro; IPR005982; Thioredox_reduct.
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu
Chen Z., Wen Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                              Read T.D., Peterson S.N., Tourses, N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinksc L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nalson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C., Hazer X.J., Cline R., Redmond C., Thwaite J.E., Nierman W.C., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         R GO; GO: 0005737; C: Cytoplasm; IEA.

GO; GO: 0005737; C: Cytoplasm; IEA.

GO; GO: 0015036; F: disulfide oxidoreductase activity; IEA.

GO; GO: 0016191; F: thioredoxin-disulfide reductase activity; IEA.

GO; GO: 0006118; P: electron transport; IEA.

GO; GO: 0019430; P: removal of superoxide radicals; IEA.

InterPro; IPR000137; Parindx reductase.

InterPro; IPR001327; Parindx reductase.

InterPro; IPR001327; Parindx reductase.

InterPro; IPR001329; Parindx reduct.

InterPro; IPR00135; Pyrredox.

InterPro; IPR00135; Pyrredox.

InterPro; IPR00193; Pyrredox.

InterPro; IPR00493; Pyrredox.

InterPro; IPR00493; Pyrredox.

InterPro; IPR00411; PNDRDTASE.

PRINTS; PR00411; PNDRDTASEI.

PRINTS; PR00411; PNDRDTASEI.

PRINTS; PR00413; PADPNY.

PRODM; PD000132; FAD. Pyrredox; 1.

RODM; PD000132; FAD. Pyrredox; 1.

PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                               "The genome's equence of Bacillus anthracis Ames and comparison to closely rome bacteria.";
Nature 423.81-86(2003).
EMBL; AE017040; AAP29046.1; -.
TIGR; BA5387; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                           MEDLINE=22608414; PubMed=12721629;
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                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-22608415; PubMed=12721630;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Ivanova N., Sorokin A., Anderson I.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,

Kapatral V., Pacten M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.;

"Genome sequence of Bacillus cereus and comparative analysis with

Bacillus anthracis.";

Nature 4338791(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE017014; AAPL2024.1; -...
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004191; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0018430; F:removal of superoxide radicals; IEA.
Interpro; IPR001327; FAD_pyr_reductase.
Interpro; IPR001327; FAD_pyr_redox.
Interpro; IPR0010100; Pyr_redox.
Interpro; IPR008255; Pyr_redox.
Interpro; IPR008255; Pyr_redox.
Interpro; IPR008255; Pyr_redox.
Interpro; IPR008255; Pyr_redox.
Interpro; IPR008255; Pyr_redox.
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                                                                                                                                Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SEOUENCE 321 AA, 34957 MW, 5B5C76F4B299D1AC CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (EC 1.6.4.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000139; FAD pyr_redox; 1.
TIGRFAMs; TIGR01292; TRX_reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00070; pyr redox; I. PRINTS; PR00419; ADXRDTASE. PRINTS; PR004119; PNDRDTASEI. PRINTS; PR00469; PNDRDTASEII.
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RGO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0019430; P:removal of superoxide radicals; IEA.
R InterPro; IPR000103; Pyridine_redox.
R InterPro; IPR000103; Pyridine_redox.
R InterPro; IPR000103; Pyridine_redox.
R InterPro; IPR001040; Pyr_redox.
R InterPro; IPR001042; Rng_mnoxygenase.
R InterPro; IPR003942; Rng_mnoxygenase.
R InterPro; IPR003942; Thioredox_reduct.
R InterPro; IPR003942; Thioredox_reduct.
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                                                                                                                                                                                                           Bacteria, Firmicutes, Bacillales, Bacillaceae, Oceanobacillus.
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-22220767, Pubmeda:12235376;
Takami H., Takaxi Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (General stress protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
A: 34337 MW; 6F0ED957848374F1 CRC64;
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                              315 AA
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                                                                 (TrEMBLrel. 23, Created)
                            PRT;
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AIKYVEDLEEKIKS 314
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                                                                                                                                                                                          Oceanobacillus iheyensis.
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Matches 217; Conservative
                        PRELIMINARY;
                                                                                                                                                                                                                                 NCBI_TaxID=182710;
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                                                                                                                                                    (EC 1.6.4.5).
OB2469.
                                                                 01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GMLPLNEAVKNLNILNDEGYIVTNEEMETSVPGIFAAGDVREKSLRQIVTATGDGSLAAQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVŢLTSTKDGSEETHEADGVEIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGTEID-FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGEEQKVYDVVIAGAGPAGMIAAVYISRANLSIVMVERGVPGGOMANTEDVENYPGFDH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

-! - COFACTOR: BA SIMILARITY).

EMBL; AP001519; BAB07290.1; -.

PIR: C84065; C84096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%; Score 1145.5; DB 16; Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R GO; GO:0005737; L'Cytcoplasm; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0005737; C:ytcoplasm; IEA.

GO; GO:00015036; F:disulfide oxidoreductase activity;

R GO; GO:00019430; P:thioredaxin-disulfide reductase activity;

R GO; GO:0019430; P:temoval of superoxide radicals; IEA.

R InterPro; IPR000159; Adrndx reductase.

InterPro; IPR000137; FAD_DYT_redox.

INTERPRO; IPR000137; FAD_DYT_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R InterPro; IPR0010109; Pyr_redox.

R PRINTS; PR00419; PNDRDTASE.

R PRINTS; PR00411; PNDRDTASE.

R TIGRRAMs; TIGR01292; TAX reduct; 1.

R PRINTS; PR00420; RNGWNOXGNASE.

R TIGRRAMs; TIGR01292; TAX reduct; 1.

R PRINTS; PR00420; RNGWNOXGNASE.

R TIGRRAMs; TIGR01292; TAX reduct; 1.

R PRINTS; PR00573; PYRIDINE REDOX 2: 1.

R PAD; Flavoprotein; Oxidoreductase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1170.2e-73;
Pred. No. 2e-73;
                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (EC 1.6.4.5)
     315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.6%; Preu. ....
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 68.6
nes 216; Conservative
                                                                                                                                                                                              Bacillus halodurans.
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TRXB OR EF1338
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01-JUN-2003 (
01-OCT-2003 (
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                                                                                                                                                           Q835N8
Q835N8;
                                                                                                                  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
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STRAIN-NCIMB 8826 / WCFS1;

STRAIN-NCIMB 8826 / WCFS1;

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,

Riefer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

A Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

A Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

De Vos W.M., Siezen R.J.;

T. Complete genome sequence of Lactobacillus plantarum WCFS1.";

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

B EBL, AL93524; CAD63354.1;

CO, GO:0015036; Frdisulfide of Conforteductase activity; IEA.

GO, GO:0015036; Frdisulfide confortase.

InterPro; IPR00137; FAD_pyr_redox.

InterPro; IPR00137; FAD_pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR00142; Mag mnoxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 943; DB 16; Length 31
55.5%; Pred. No. 4.9e-59;
ive 54; Mismatches 83; Indels
                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (EC 1.6.4.5).
TRXBI OR LP 0761.
Lactobacillus plantarum.
Bactoria; Firmicutes; Lactobacillales; Lactobacillus.
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERMITS, PRO0070; PYT_redox; 1.

PRINTS; PRO0419; ADXRDTASE.

PRINTS; PRO0469; PADPUT.

PRINTS; PRO0469; PNDRDTASEII.

PRINTS; PRO0420; RNGMNOXGNASE.

PROSTITS; PRO0420; RNGMNOXGNASE.

COXidoreductase; Complete proteome.

SEQUENCE 312 AA; 33455 MW; BF013DD361EDB343 CRC64;
                                                                                                                                                                     312 AA
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 55.5%;
                                                   301 NVOHYIEELAEKVKN 315
         300 SAAEYIEHLNDQARS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 171; Conservative
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1590;
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                                                                                                                            RESULT 9
                                                                                                                                                       28877
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ODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KMYENVEKFGTENAYGIVMGIEDHGSYKEVICDDKSYEAKAVIIATGCEHRKLGVKGEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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STRAIN-V583 / ATCC 700802;

MEDLINE-22550857; PubMed=12663927;

MEDLINE-22550857; PubMed=12663927;

Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,

Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,

Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.,

"Role of mobile DNA in the evolution of vancomycin-resistant

Science 299:2071-2074(2003).
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R TIGR; EF1338; -.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:00015737; C:cytoplasm; IEA.

GO; GO:000191; F:thioredoxin-disulfide reductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0019430; P:electron transport; IEA.

R InterPro; IPR001327; FAD pyr_redox.

R InterPro; IPR001327; FAD pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Thioredox_reduct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AA; 33240 MW; F08B31A3E28628EE CRC64;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Mismatches
                                                                                                                                                                                     304 AA.
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPIR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
PRODOM; PD001039; PAD_pyr_redox; 1.
PTGRFAMS; TIGR01292; TRX_reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                        (TrEMBLrel. 24, (TrEMBLrel. 24, (TrEMBLrel. 25,
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Best Local Similarity 58.9%,
Matches 178; Conservative
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                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           Thioredoxin reductase.
307 HINDQARS 314
                                                     305 ALGDKVNN 312
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SEQUENCE 304 AA
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NCBI_TaxID=198466;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            emergence.
                                                                                                                                                                                                                                                                                   Q8K6D2
Q8K6D2;
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Matches
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                                             247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
182 QDRAFANEKISFVWDTVVEEIVGNEMVVTGVKARNVKTDEVSEIEANGVFIYVGLDPLTE 241
                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
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                                                                    7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGPDLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

R EMBL, ABG10078; AAL98210.1; -...
GO, GO:0005737; C:vycpplasm; IEA.
GO, GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004930; F:electron transport; IEA.
IN GO; GO:0019430; P:removal of superoxide radicals; IEA.
InterPro; IPR000139; Pardada reductase.
InterPro; IPR000139; Pardida redox.2.
InterPro; IPR000130; Pyridine_redox.2.
InterPro; IPR008255; Pyr_redox.
R InterPro; IPR008255; Pyr_redox.
R InterPro; IPR008255; Pyr_redox.
R InterPro; IPR008255; Pyr_redox.
R InterPro; IPR008255; Pyr_redox.
R PrincerPro; IPR008255; Pyr_redox.
R PrincerPro; IPR008255; Pyr_redox.
R PrincerPro; IPR008255; Pyr_redox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus Pyogenes (serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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56.3%; Pred. No. 6.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRO0411; PNDRDTASEI.
PRINTS, PR00469; PNDRDTASEII.
TIGREAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00070; DYr redox; 1
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
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Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                 307 HL 308
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RP SEQUENCE FROM N.A.

RP STRAIN=SSI-1 / Serotype M3;

RA Arazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,

RA Arazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,

RA Hayashi H., Hamada S.;

RT Senome of invasive Streptococcus pyogenes; a comparative analysis of S. Pyogenes SSI-1, SR370 and MGAS8332.";

RI Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RB Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RB SCH SENDIA: ABOG142; BAC63562.1;

RB SENDIA: ABOG142; BAC63562.1;

RG SO CO0005737; C:cytoplasm; IEA.

BR GO; GO:00064791; F:peroxidase activity; IEA.

GO; GO:0004791; F:peroxidase activity; IEA.

BR GO; GO:001470; P:thioredoxin-disulfide reductase activity; IEA.

BR GO; GO:001470; P:thioredoxin-disulfide radicals; IEA.

BR GO; GO:001470; P:thioredoxin-disulfide radicals; IEA.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00100; Pyr redox_2.

BR RINTS; PR0041; PNDRDIASEI.

BRINTS; PR0041; PNDRDIASEI.

BR RINTS; PR0041; PNDRDIASEI.

BR PRINTS; PR0041; PNDRDIASEI.

BR PRINTS; PR0041; PNDRDIASEI.

BR PRINTS; PR00419; ADAXDIASEI.

BR PRINTS; PR00419; PNDRDIASEI.
                                                                                                                                                            306
187 ODRAFKNDKIDFIWSHTTKSINEKDGKVGSVILTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                           242 MVKDLEITDSEGWIITDDHMRTSIPGIFALGDVRQKDLRQIITAVGDGAIAGGGVYYYLE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                  247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative thioredoxin reductase (Putative NADH oxidase/alkyl
hydroperoxidase reductase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREPANS; TIGRO1292; TRX reduct; 1.
PROSITE; PSO0573; PYRIDINE REDOX 2; 1.
Hypothetical protein; Peroxidase; Complete proteome.
SEQUENCE 305 AA; 33543 MW; 3F947A628769EBBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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                                                                                                                                                                                                                                                                                                                                                                                             305 AA
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOX.2 OR SPYM3_1395 OR SPS0467.
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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DLSTRMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                  187 ODRAFKNDKIDFIWSHTIKSINEKDGKVGSVILISIKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                            182 ÓEKAFANDKVDFIMDSVVKEIKGNDLKVTNVDIENVKTGOVNNYAFGGVFIYVGLDPVSS 241
                              62 KMHBPLEKFGVENLYGIVTAVEDHGNFKKVLTDDNSYETKIVIIATGAKHRPLAVAGEET 121
                                                                                                                                                                                                                                                                         247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYI 305
                                                                                                                                                                                                                                                                                                  3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                     127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
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    KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0005737; C:cytoplasm; IEA.
GO, GO:0005737; C:cytoplasm; IEA.
GO, GO:0015035; F:disulfide oxidoreductase activity; IEA.
GO, GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO, GO:0006118; P:electron transport; IEA.
GO, GO:0019430; P:electron transport; IEA.
InterPro; IPR00130; P:redox.
InterPro; IPR00137; FAD pyr_redox.
InterPro; IPR001010; Pyr Iredox.
InterPro; IPR001855; Pyr_redox.
InterPro; IPR008255; Pyr_redox.
InterPro; IPR008255; Pyr_redox.
InterPro; IPR008255; Pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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PRINTS; PR00469; PNDRDTASEII.

TIGREAMS; TIGR01292; TRX reduct; 1.

PROSTIE; PS00673; PYRIDINE REDOX 2; 1.

FAD; Flavoprotein; Oxidoreductase; Complete proteome.

SEQUENCE 308 AA; 33894 MW; 363397A925E48267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Thioredoxin reductase (BC 1.6.4.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21235186; PubMed=11337471;
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
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Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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HSSP; Q39243; 1VDC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-IL1403;
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Q9CH02
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                                                                                                                                                                               186
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                                                                                                                                                                                                                                                                                                                                                             247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                       KMFEHAKKEGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 126
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  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                         2 YDTLIIGSGPAGMTAALYAARSNLSVAIIEQGAPGGOMNTFDIENYPGYDHISGPELAM
                                                                                                                  127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
                                                                                                                                                                                                       QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA
                                                                                                                                                                                                                                                                                                Gaps
FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patuogen. 1

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

R EMBL; AE014892; AANSB212.1; -...

R GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0006718; F:disulfide oxidoreductase activity; IEA.

RO; GO:0006118; P:thioredoxin-disulfide reductase activity; IEA.

R GO; GO:0006118; P:thioredoxin-disulfide reductase activity; IEA.

R O; GO:0006118; P:electron transport; IEA.

R InterPro; IPR000759; Adrindx reductase.

R InterPro; IPR000137; FAD pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEF7BEC1BE80A50F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ol-CCT-2003 (TrEMBLrel. 23, Last sequence update)
Ol-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative thioredoxin reductase (NADPH) (EC 1.6.4.5)
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STRAIN-UA159 / ATCC 700610 / Serotype C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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PROSTIE; PS00573; PYRIDINE REDOX 2; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 304 Aa; 33117 MW; CBF7BEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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NCBI_TaxID=1309;
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01-MAR-2003
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QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
                                                                                                                      PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                                                                                                                                                                                                                                                                        GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-NEM316 / Serotype III;
STRAIN-NEM316 / Serotype III;
STRAIN-E-22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek_T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO:005737; C:ytoplasm; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R InterPro; IPR0001327; FAD:pyr_redox.

InterPro; IPR001327; FAD:pyr_redox.

InterPro; IPR001327; FAD:pyr_redox.

InterPro; IPR001355; Pyr_redox.

InterPro; IPR001355; Pyr_redox.

InterPro; IPR005982; Thioredox_reduct.

R Ffam; PF00070; pyr_redox; 1.

R PRINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRINTS; PRO0401; PNDEDTASEI.
PRINTS; PR00406; PNDEDTASEII.
TIGREAMS; TIGR01292; TRX reduct; 1.
TIGREAMS; TIGR01292; TRX reduct; 1.
HYPOTHETICAL Protein; Complete proteome.
SEQUENCE 304 AA; 33123 MW; 4B6B55E55FB84EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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53.3%; Pred. No. 1.3e-52;
ive 57; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AA
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EMBL; AL766844; CAD45929.1;
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23,
25,
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Mol. Microbiol. 45:1499-15
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NCBI_TaxID=216495;
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01-MAR-2003 (
01-OCT-2003 (
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Best Local
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